

SEQUENCE LISTING

RECEIVED
OCT 27 2003
TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BURLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna Pieterella
LAGEWEG, Wessel
PONSTEIN, Anne Silene
LAGEWEG, Wessel
PONSTEIN, Anne Silene

(ii) TITLE OF INVENTION: ANTIFUNGAL PROTEINS, DNA CODING THEREFORE,
AND HOSTS INCORPORATING SAME.

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: LADAS & PARRY
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(v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: 3.25" Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: WINDOWS 95
(D) SOFTWARE: WORDPERFECT 8

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/258,031
(B) FILING DATE: 25-FEB-1999
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP97/04923
(B) FILING DATE: 04-SEP-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP97200831.2
(B) FILING DATE: 19-MAR-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP96202466.7
(B) FILING DATE: 04-SEP-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helianthus annuus
 - (B) STRAIN: cv. zebulon
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly
 1 5 10 15

Ala Thr Leu Gly Glu Val Tyr Tyr Arg
 20 25

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helianthus annuus
 - (B) STRAIN: cv. zebulon
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Xaa Ser
 1 5 10 15

Ser Phe Pro Thr Val Leu Gln Asn Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCTCCN AGNGTNGCNC CNGCTTGNAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCNTCTT TCCCNATTAC TGGNGAGGTT TA

32

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helianthus annuus*
 (B) STRAIN: cv. zebulon

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAT CCG TCT TTC CCG ATT ACT GGG GAG GTT TAC ACT CCC GGA AAC TCA	48
Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser	
1 5 10 15	
TCT TTT CCT ACC GTC TTG CAA AAC TAC ATC CGA AAC CTT CGG TTC AAT	96
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn	
20 25 30	
GAA ACT ACC ACA CCA AAA CCC TTT TTA ATC ATC ACA GCC GAA CAT GTT	144
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val	
35 40 45	
TCC CAC ATT CAG GCA GCT GTG GTT TGT GGC AAA CAA AAC CGG TTG CTA	192
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu	
50 55 60	
CTG AAA ACC AGA AGC GGT GGT CAT GAT TAT GAA GGT CTT TCC TAC CTT	240
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu	
65 70 75 80	
ACA AAC ACA AAC CAA CCC TTC TTC ATT GTG GAC ATG TTC AAT TTA AGG	288
Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg	
85 90 95	
TCC ATA AAC GTA GAT ATC GAA CAA GAA ACC GCA TGG GTC CAA GCC GGC	
336	
Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly	
100 105 110	
GCC ACC CTC GGA GAA GTT	354
Ala Thr Leu Gly Glu Val	
115	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser
1 5 10 15
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn
20 25 30
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val
35 40 45
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu
50 55 60
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu
65 70 75 80
Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg
85 90 95
Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly
100 105 110
Ala Thr Leu Gly Glu Val
115

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCAGCTG TGTTTTGTGG C

21

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTCCACAATG AAGAAGGGTT G

21

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACGTAGATAT CGAACAAGAA ACCGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GCTTTACTAC ACGGGCTTCC CCAG

24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTGGGGAAGC CCGTGTAGTA AAGC

24

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTACTCCAA CCACGGCGCT C

21

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGGAAGTTG CAGAAGATTG GGTG

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GAGCAAGAGA AGAAGGAGAC

20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1784 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helianthus annuus

(B) STRAIN: Zebulon

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 21..1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATATCACATC TTCTTTCAAC ATG CAA ACT TCC ATT CTT ACT CTC CTT CTT

50

Met Gln Thr Ser Ile Leu Thr Leu Leu Leu																		
					1						5						10	
CTC	TTG	CTC	TCA	ACC	CAA	TCT	TCT	GCA	ACT	TCC	CGT	TCC	ATT	ACA	GAT		98	
Leu	Leu	Leu	Ser	Thr	Gln	Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp			
				15					20					25				
CGC	TTC	ATT	CAA	TGT	TTA	CAC	GAC	CGG	GCC	GAC	CCT	TCA	TTT	CCG	ATA		146	
Arg	Phe	Ile	Gln	Cys	Leu	His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile			
				30					35					40				
ACC	GGA	GAG	GTT	TAC	ACT	CCC	GGA	AAC	TCA	TCT	TTT	CCT	ACC	GTC	TTG		194	
Thr	Gly	Glu	Val	Tyr	Thr	Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu			
				45					50					55				
CAA	AAC	TAC	ATC	CGA	AAC	CTT	CGG	TTC	AAT	GAA	ACT	ACC	ACA	CCA	AAA		242	
Gln	Asn	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys			
				60					65					70				
CCC	TTT	TTA	ATC	ATC	ACA	GCC	GAA	CAT	GTT	TCC	CAC	ATT	CAG	GCA	GCT		290	
Pro	Phe	Leu	Ile	Ile	Thr	Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala			
				75					80					85				
GTG	GTT	TGT	GGC	AAA	CAA	AAC	CGG	TTG	CTA	CTG	AAA	ACC	AGA	AGC	GGT		338	
Val	Val	Cys	Gly	Lys	Gln	Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly			
				95					100					105				
GGT	CAT	GAT	TAT	GAA	GGT	CTT	TCC	TAC	CTT	ACA	AAC	ACA	AAC	CAA	CCC		386	
Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro			
				110					115					120				
TTC	TTC	ATT	GTG	GAC	ATG	TTC	AAT	TTA	AGG	TCC	ATA	AAC	GTA	GAT	ATC		434	
Phe	Phe	Ile	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile			
				125					130					135				
GAA	CAA	GAA	ACC	GCA	TGG	GTC	CAA	GCC	GGT	GCG	ACT	CTT	GGT	GAA	GTG		482	
Glu	Gln	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val			
				140					145					150				
TAC	TAT	CGA	ATA	GCG	GAG	AAA	AGT	AAC	AAG	CAT	GGT	TTT	CCG	GCA	GGG		530	
Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly			
				155					160					165				
GTT	TGT	CCA	ACG	GTT	GGC	GTT	GGT	GGG	CAT	TTT	AGT	GGT	GGT	GGG	TAT		578	
Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr			
				175					180					185				
GGT	AAT	TTG	ATG	AGA	AAA	TAT	GGT	TTG	TCG	GTT	GAT	AAT	ATT	GTT	GAT		626	
Gly	Asn	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp			
				190					195					200				
GCT	CAA	ATA	ATA	GAT	GTG	AAT	GGC	AAG	CTT	TTG	GAT	CGA	AAG	AGT	ATG		674	
Ala	Gln	Ile	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met			
				205					210					215				

GGT GAG GAT TTG TTT TGG GCG ATC ACC GGC GGT GGT GGT GTT AGT TTT	722
Gly Glu Asp Leu Phe Trp Ala Ile Thr Gly Gly Gly Gly Val Ser Phe	
220 225 230	
GGT GTG GTT CTA GCC TAC AAA ATC AAA CTA GTT CGT GTT CCG GAG GTT	770
Gly Val Val Leu Ala Tyr Lys Ile Lys Leu Val Arg Val Pro Glu Val	
235 240 245 250	
GTG ACC GTG TTT ACC ATT GAA AGA AGA GAG GAA CAA AAC CTC AGC ACC	818
Val Thr Val Phe Thr Ile Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr	
255 260 265	
ATC GCG GAA CGA TGG GTA CAA GTT GCT GAT AAG CTA GAT AGA GAT CTT	866
Ile Ala Glu Arg Trp Val Gln Val Ala Asp Lys Leu Asp Arg Asp Leu	
270 275 280	
TTC CTT CGA ATG ACC TTT AGT GTC ATA AAC GAT ACC AAC GGT GGA AAG	914
Phe Leu Arg Met Thr Phe Ser Val Ile Asn Asp Thr Asn Gly Gly Lys	
285 290 295	
ACA GTC CGT GCT ATC TTT CCA ACG TTG TAC CTT GGA AAC TCG AGG AAT	962
Thr Val Arg Ala Ile Phe Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn	
300 305 310	
CTT GTT ACA CTT TTG AAT AAA GAT TTC CCC GAG TTA GGG TTG CAA GAA	1010
Leu Val Thr Leu Leu Asn Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu	
315 320 325 330	
TCG GAT TGT ACT GAA ATG AGT TGG GTT GAG TCT GTG CTT TAC TAC ACG	1058
Ser Asp Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr	
335 340 345	
GGC TTC CCC AGT GGT ACT CCA ACC ACG GCG CTC TTA AGC CGT ACT CCT	1106
Gly Phe Pro Ser Gly Thr Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro	
350 355 360	
CAA AGA CTC AAC CCA TTC AAG ATC AAA TCC GAT TAT GTG CAA AAT CCT	1154
Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro	
365 370 375	
ATT TCT AAA CGA CAG TTC GAG TTC ATC TTC GAA AGG CTG AAA GAA CTT	1202
Ile Ser Lys Arg Gln Phe Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu	
380 385 390	
GAA AAC CAA ATG TTG GCT TTC AAC CCA TAT GGT GGT AGA ATG AGT GAA	1250
Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu	
395 400 405 410	
ATA TCC GAA TTC GCA AAG CCT TTC CCA CAT AGA TCG GGT AAC ATA GCG	1298
Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser Gly Asn Ile Ala	
415 420 425	
AAA ATT CAA TAC GAA GTA AAC TGG GAG GAT CTT AGC GAT GAA GCC GAA	1346
Lys Ile Gln Tyr Glu Val Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu	

430	435	440	
AAT CGT TAC TTG AAT TTC ACA AGG CTG ATG TAT GAT TAC ATG ACC CCA			1394
Asn Arg Tyr Leu Asn Phe Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro			
445	450	455	
TTT GTG TCG AAA AAC CCT AGA AAA GCA TTT TTG AAC TAT AGG GAT TTG			1442
Phe Val Ser Lys Asn Pro Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu			
460	465	470	
GAT ATT GGT ATC AAC AGC CAT GGC AGG AAT GCT TAT ACT GAA GGA ATG			1490
Asp Ile Gly Ile Asn Ser His Gly Arg Asn Ala Tyr Thr Glu Gly Met			
475	480	485	490
GTT TAT GGG CAC AAG TAT TTC AAA GAG ACA AAT TAC AAG AGG CTA GTA			1538
Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val			
495	500	505	
AGT GTG AAG ACT AAA GTT GAT CCT GAC AAC TTC TTT AGG AAT GAG CAA			1586
Ser Val Lys Thr Lys Val Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln			
510	515	520	
AGC ATC CCA ACT TTG TCA TCT T GAAGAACGTA CATATATAAA TAAATACCTT			1638
Ser Ile Pro Thr Leu Ser Ser			
525			
TGTGCATGGT ATTTTCAGGG TGTTAAAGTG ATATTCAGAT ATTTATGATA GAATTTTGAC			1698
TTGTATTTTA TACAATCAAA ATTGTATGGT TCTCCGAATT TCTCTTTTTA ATTCTGAAAA			1758
ATACATATTA GTATTGTCAA AAAAAA			1784

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Gln	Thr	Ser	Ile	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Ser	Thr	Gln	
1				5				10					15		
Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp	Arg	Phe	Ile	Gln	Cys	Leu
		20					25					30			
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr
		35					40				45				
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn

50					55					60					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr
65					70					75					80
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln
				85					90					95	
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly
			100					105					110		
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met
		115					120					125			
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp
	130					135					140				
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu
145					150					155					160
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly
				165					170					175	
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys
			180					185					190		
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val
		195					200					205			
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp
	210					215					220				
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr
225						230					235				240
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile
				245					250					255	
Glu	Arg	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val
			260					265					270		
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe
		275					280					285			
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe
		290					295					300			
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn
305						310					315				320
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met
				325					330					335	
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr

340	345	350
Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe		
355	360	365
Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro Ile Ser Lys Arg Gln Phe		
370	375	380
Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu Glu Asn Gln Met Leu Ala		
385	390	395
Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu Ile Ser Glu Phe Ala Lys		
405	410	415
Pro Phe Pro His Arg Ser Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val		
420	425	430
Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu Asn Arg Tyr Leu Asn Phe		
435	440	445
Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro		
450	455	460
Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser		
465	470	475
His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr		
485	490	495
Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val		
500	505	510
Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser		
515	520	525
Ser		

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGCCATGGA GACTTCCATT CTTACTC

27

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCGGATCCT CAAGATGACA AAGTTGGGAT GCT

33

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helianthus annuus*
- (B) STRAIN: Zebulon

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG GAG ACT TCC ATT CTT ACT CTC CTT CTT CTC TTG CTC TCA ACC CAA 48
Met Glu Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Leu Ser Thr Gln
1 5 10 15

TCT TCT GCA ACT TCC CGT TCC ATT ACA GAT CGC TTC ATT CAA TGT TTA 96
Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp Arg Phe Ile Gln Cys Leu

20					25					30						
CAC	GAC	CGG	GCC	GAC	CCT	TCA	TTT	CCG	ATA	ACC	GGA	GAG	GTT	TAC	ACT	144
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr	
		35					40					45				
CCC	GGA	AAC	TCA	TCT	TTT	CCT	ACC	GTC	TTG	CAA	AAC	TAC	ATC	CGA	AAC	192
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn	
	50					55					60					
CTT	CGG	TTC	AAT	GAA	ACT	ACC	ACA	CCA	AAA	CCC	TTT	TTA	ATC	ATC	ACA	240
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr	
	65				70					75					80	
GCC	GAA	CAT	GTT	TCC	CAC	ATT	CAG	GCA	GCT	GTG	GTT	TGT	GGC	AAA	CAA	288
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln	
				85				90						95		
AAC	CGG	TTG	CTA	CTG	AAA	ACC	AGA	AGC	GGT	GGT	CAT	GAT	TAT	GAA	GGT	336
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	
		100						105					110			
CTT	TCC	TAC	CTT	ACA	AAC	ACA	AAC	CAA	CCC	TTC	TTC	ATT	GTG	GAC	ATG	384
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met	
		115					120					125				
TTC	AAT	TTA	AGG	TCC	ATA	AAC	GTA	GAT	ATC	GAA	CAA	GAA	ACC	GCA	TGG	432
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp	
	130					135					140					
GTC	CAA	GCC	GGT	GCG	ACT	CTT	GGT	GAA	GTG	TAC	TAT	CGA	ATA	GCG	GAG	480
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	
	145				150					155					160	
AAA	AGT	AAC	AAG	CAT	GGT	TTT	CCG	GCA	GGG	GTT	TGT	CCA	ACG	GTT	GGC	528
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	
				165				170						175		
GTT	GGT	GGG	CAT	TTT	AGT	GGT	GGT	GGG	TAT	GGT	AAT	TTG	ATG	AGA	AAA	576
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys	
			180					185					190			
TAT	GGT	TTG	TCG	GTT	GAT	AAT	ATT	GTT	GAT	GCT	CAA	ATA	ATA	GAT	GTG	624
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val	
		195					200					205				
AAT	GGC	AAG	CTT	TTG	GAT	CGA	AAG	AGT	ATG	GGT	GAG	GAT	TTG	TTT	TGG	672
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	
	210					215					220					
GCG	ATC	ACC	GGC	GGT	GGT	GGT	GTT	AGT	TTT	GGT	GTG	GTT	CTA	GCC	TAC	720
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr	
	225				230					235					240	

AAA ATC AAA CTA GTT CGT GTT CCG GAG GTT GTG ACC GTG TTT ACC ATT	768
Lys Ile Lys Leu Val Arg Val Pro Glu Val Val Thr Val Phe Thr Ile	
245 250 255	
GAA AGA AGA GAG GAA CAA AAC CTC AGC ACC ATC GCG GAA CGA TGG GTA	816
Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr Ile Ala Glu Arg Trp Val	
260 265 270	
CAA GTT GCT GAT AAG CTA GAT AGA GAT CTT TTC CTT CGA ATG ACC TTT	864
Gln Val Ala Asp Lys Leu Asp Arg Asp Leu Phe Leu Arg Met Thr Phe	
275 280 285	
AGT GTC ATA AAC GAT ACC AAC GGT GGA AAG ACA GTC CGT GCT ATC TTT	912
Ser Val Ile Asn Asp Thr Asn Gly Gly Lys Thr Val Arg Ala Ile Phe	
290 295 300	
CCA ACG TTG TAC CTT GGA AAC TCG AGG AAT CTT GTT ACA CTT TTG AAT	960
Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn Leu Val Thr Leu Leu Asn	
305 310 315 320	
AAA GAT TTC CCC GAG TTA GGG TTG CAA GAA TCG GAT TGT ACT GAA ATG	1008
Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu Ser Asp Cys Thr Glu Met	
325 330 335	
AGT TGG GTT GAG TCT GTG CTT TAC TAC ACG GGC TTC CCC AGT GGT ACT	1056
Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr Gly Phe Pro Ser Gly Thr	
340 345 350	
CCA ACC ACG GCG CTC TTA AGC CGT ACT CCT CAA AGA CTC AAC CCA TTC	1104
Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe	
355 360 365	
AAG ATC AAA TCC GAT TAT GTG CAA AAT CCT ATT TCT AAA CGA CAG TTC	1152
Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro Ile Ser Lys Arg Gln Phe	
370 375 380	
GAG TTC ATC TTC GAA AGG ATG AAA GAA CTT GAA AAC CAA ATG TTG GCG	1200
Glu Phe Ile Phe Glu Arg Met Lys Glu Leu Glu Asn Gln Met Leu Ala	
385 390 395 400	
TTC AAC CCA TAT GGT GGT AGA ATG AGT GAA ATA TCC GAA TTC GCA AAG	1248
Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu Ile Ser Glu Phe Ala Lys	
405 410 415	
CCT TTC CCA CAT AGA TCG GGT AAC ATA GCG AAG ATT CAA TAC GAA GTA	1296
Pro Phe Pro His Arg Ser Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val	
420 425 430	
AAC TGG GAG GAT CTT AGC GAT GAA GCC GAA AAT CGT TAC TTG AAT TTC	1344
Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu Asn Arg Tyr Leu Asn Phe	
435 440 445	
ACA AGG CTG ATG TAT GAT TAC ATG ACT CCA TTT GTG TCG AAA AAC CCT	1392

Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro
 450 455 460

AGA GAA GCA TTT TTG AAC TAT AGG GAT TTG GAT ATT GGT ATC AAC AGC 1440
 Arg Glu Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser
 465 470 475 480

CAT GGC AGG AAT GCT TAT ACT GAA GGA ATG GTT TAT GGG CAC AAA TAT 1488
 His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr
 485 490 495

TTC AAA GAG ACA AAT TAC AAG AGG CTA GTA AGT GTG AAG ACT AAA GTT 1536
 Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val
 500 505 510

GAT CCT GAC AAC TTC TTT AGG AAT GAG CAA AGC ATC CCA ACT TTG TCA 1584
 Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser
 515 520 525

TCT TG 1589
 Ser
 530

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Glu Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Ser Thr Gln
 1 5 10 15
 Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp Arg Phe Ile Gln Cys Leu
 20 25 30
 His Asp Arg Ala Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr
 35 40 45
 Pro Gly Asn Ser Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn
 50 55 60
 Leu Arg Phe Asn Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr
 65 70 75 80
 Ala Glu His Val Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln
 85 90 95

Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	100	105	110
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met	115	120	125
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp	130	135	140
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	145	150	155
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	165	170	175
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys	180	185	190
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val	195	200	205
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	210	215	220
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr	225	230	235
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile	245	250	255
Glu	Arg	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val	260	265	270
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	275	280	285
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe	290	295	300
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn	305	310	315
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met	325	330	335
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr	340	345	350
Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg	Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	355	360	365
Lys	Ile	Lys	Ser	Asp	Tyr	Val	Gln	Asn	Pro	Ile	Ser	Lys	Arg	Gln	Phe	370	375	380

Glu	Phe	Ile	Phe	Glu	Arg	Met	Lys	Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	385		390		395		400
Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met	Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys		405		410		415	
Pro	Phe	Pro	His	Arg	Ser	Gly	Asn	Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val		420		425		430	
Asn	Trp	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Glu	Asn	Arg	Tyr	Leu	Asn	Phe		435		440		445	
Thr	Arg	Leu	Met	Tyr	Asp	Tyr	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	450		455		460		
Arg	Glu	Ala	Phe	Leu	Asn	Tyr	Arg	Asp	Leu	Asp	Ile	Gly	Ile	Asn	Ser	465		470		475		480
His	Gly	Arg	Asn	Ala	Tyr	Thr	Glu	Gly	Met	Val	Tyr	Gly	His	Lys	Tyr		485		490		495	
Phe	Lys	Glu	Thr	Asn	Tyr	Lys	Arg	Leu	Val	Ser	Val	Lys	Thr	Lys	Val		500		505		510	
Asp	Pro	Asp	Asn	Phe	Phe	Arg	Asn	Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser		515		520		525	

Ser

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..350
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAGAAACTCG GAGACTTTCA CACAATGCCT AACCTCAAAC TCCGACCCCA AACATCCCAT 60
 CTCCCCCGCT ATCTTCTTCT CCGGAAATGG CTCCTACTCC TCCGTATTAC AAGCCAACAT 120
 CCGTAACCTC CGCTTCAACA CCACCTCAAC TCCGAAACCC TTCCTCATAA TCGCCGCAAC 180
 ACATGAATCC CATGTGCAAG CCGCGATTAC TTGCGGGAAA CGCCACAACC TTCAGATGAA 240
 AATCAGAAGT GGAGGCCACG ACTACGATGG CTTGTCATAC GTTACATACT CTGGCAAACC 300
 GTTCTTCGTC CTCGACATGT TTAACCTCCG TTCGGTGGAT GTCGACGTGG 350

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGCATGGATC TCCGCCGAG CGACTCTCGG AGAGGTTTAT TATCGGATTT GGGAGAAAAG 60
 CAGAGTCCAT GGATTCCCCG CCGGAGTTTG ACCGACGGTT GGTGTTGGTG GGCATTTAAG 120
 CGGCGGTGGT TACGGTAACA TGGTGAGGAA GTTTGGATTA TCTGTGGATT ACGTTGAGGA 180
 TGCCAAGATC GTCGATGTAA ACNGTCGGGT TTTAGATCGG AAAGCAATGG GTGAGGATCT 240
 GTTCTGGGCG ATTACCGGTG GAGGAGGAGG TAGCGTAC 278

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
TGGACATATT AGCGGAGGAG GATTCGGTAC AATAATGAGG AAATACGGTT TAGCGTCTGA 60
TAACGTTGTG GACGCACGTT TGATGGATGT AAATGGGAAA ACTCTTGACC GGAAAACGAT 120
GGGAGAGGAT TTGTTTTGGG CGCTTAGAGG CGGTGGAGCT GCGAGTTTTG GCGTTGTCTT 180
GTCGTGGAAG GTTAAGCTTG CTAGGGTTCC TGAAAAGGTA ACTTGTTTCA TAAGTCAACA 240
TCCGATGGGA CCTAGCATGA ACAAGCTTGT TCATAGATGG CAATCCATAG GATCAAGANN 300
GCTAGACGAA GATTATTCA TCAGAGTCAA TATTGACAAC AGTCT 345
```

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..695
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTCGTTAAA ACCTATCCTN NANGGGCNAA AGNATATCAA AGNTTGNTTA NGNAACCCAA 60
 NATTTCTGAA CTGGCCNCCT TCGGTGGTAT ATGNCNAAAN CCCTTGAATC TGCGNANCCN 120
 ATTCCGCATA GAAACGGAAC CCTCTTCAAG ATTCTCTATT TACNCGAACT GNCTAGANNG 180
 AATGACAAGA CATCGAGTAG NAAAATCAAC TGGATCAAAG AGATATACAA TTACATGGCG 240
 CCTTATGTCT CAAGCAATCC AAGACAAGCA TATGTGAACT ACAGAGATCT AGACTTCGGA 300
 CAGAACAAGA ACAACGCAAA GGTTAACTTC ATTGAAGCTA AAATCTGGGG ACCTAAGTAC 360
 TTCAAAGGCA ATTTTGACAG ATTGGTGAAG ATTAAAACCA AGGTTGATCC AGAGAACTTC 420
 TTCAGGCACG AGCAGAGTAT CCCACCTATG CCCTACTAGA AGCTAGGTTT ATGAAACCAA 480
 TAACATTATC AAAAATAAGR ATAAATGRTA ATTGTATACA ACATGATTCG KCTTTCTTTA 540
 TTTCAGACAA TGTGGACACT ACTCTAAANT AAAAWGTCNA TTTACCTTAA AAAAAAATA 600
 ATCCCNNTA ANANAAAANT GGGGGGGCCN TTTTGGGGN TCCCGGTTTT NGGACGGGGN 660
 GCTTTNGGGG GGCTTGGNNT TTTTTTNGGN GCCCC 695

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCTGTTTTNA GGCAGAGCAG AGGAAGTTGT TGCTTTGCTT GGTAAGGAGT TTCCTGAATT 60
 NAGTTTAAAG AAGGAGAACT GTTCGGAGAT GACTTGGTTT CAGTCAGCTT TATGGTGGGA 120
 TAATCGTGTT AACCTACTC ANATTGATCC WAAAGTGTTT CTCGATCGGA ATCTTGATAG 180

```

AGCGAATTTTC GGAAAGAGGA AATCGGATTA CGTTGCGAGT AAGATTCCTA GAGATGGGAT 240
TAAGYCTTTT TCCAAGARGA TGMCTGACCT GGGGAAAAYC GGGCTTGTTT TTAAWCCGTA 300
TGGTGGGAAA ATGGCGGAGG TTACGGTTAA CGCGACGCCG TTCCNCACC GAAGCAAGCT 360
TTTTAAGATT CAGTACTCGG TGACTIONGCA AGAAAACCTCT NTCGAGATAG AGAAAGGGTT 420
TCTTGAATCA GGCTAACGTC CTTATAGGTT CATGACCGGG TTTTNNAGCA AGANCCCTGG 480
AATNCTTACT TNAAT

```

495

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

AAATTAAAAC AAATCAATGT TGATATTGAA TCCAATAGTG CTTGGTTTCA ACCTGGTGCT 60
ACGCTTGGTG AGCTTTACTA CAGAATTNCA GAGAAGAGCA AAATCCATGG ATTTCCNGCG 120
GGTTTNTNCA CAAGCNTAGG CATAGGTGGG TATATNANAG GCGGTGGATA CGGTACCTTG 180
ATGAGGAAGT ATGGTCTTNC GGGA

```

204

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

GAGATTTCTC GAGCAAGATA CTCCACTGAT GATCTTTGAG CCATTGGGTG GGAAAATCAG 60
CAAGATTTCA GAAACAGAAT CTCCATATCC ACACAGAAGA GGTAATCTGT ATAATATACA 120
GTACATGGTG AAATGGAAAG TGAATGANGT CGAGGAGATG AACAAACATG TCAGGTGGAT 180
GAGATCGTTA CACGATTACA TGA CTCCGTA TGTTTCTAAA TCGCCGAGAG GAGCTTATTT 240
GANTTACAGA GATCTTGATT TGGGCTCGAC CAAAGGGATT AACACGGGTT TCGGAGATGC 300
AAGGAAATGG NNGGGTGAGN CTTTTTTTCAA AGGTAATTTT CAAGGGGTTA GGTTTTGGTT 360
AAAGGGGAGG TTTNNCCCAN CAAATTTTTTT TTCAGGANCC GGCCANGNTT TTCCCCCCCC 420
TNTTTTTTNGG NCCCCAATCN AAANCCCCGT TTTAAAAGGG GGGCCATTTC NTTTTTTNCA 480
NNTTAAAAGG G 491

```

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
ATTTGTTCTGT GAGGTTAACT TTGACTTTAG TCAACGGTAC GAAGCCTGGT GAGAATACGG 60
TTTtagCGAC TTTCATTGGG ATGTATTTAG GCCGGTCGGA TAAGCTGTTG ACCGTNATGA 120
ACCGGGATTT CCCGGAGTTG AAGCTGAAGA AAACCGATTN TACCGAGATG AGATGGATCG 180
ATTCGGTTCT GTTTTGGGAC GATTATCCGG TTGGTACACC GACTTCTGTG CTACTAAATC 240
CGCTAGTCGC AAAAAAGTTG TTCATGAAAC GAAAATCGGA CTACGTGAAG CGTCTNATTT 300
TCGAGAACCC GATCTCNNGT TTGATACTCA AGAAATTTGT AGAGGTTNNG AAAGTTAAAA 360
TNAATTTGGA TCCGCATTNN GGNANNNATG GTGAAACCCC NNGTTNT 407
```

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*
(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
ACGGCGTCGT ATTGGCCTAC AAAATAAACC TTGTTGAAGT CCCAGAAAAC GTCACCGTTT 60
TCAGAATCTC CCGGACGTTA GAACAAAATG CGACGGATAT CATTACCGG TGGCAACAAG 120
TTGCACCGAA GCTTCCCGAC GAGCTTTTCA TAAGANCAGT CATTGACGTA NAAACGGCAC 180
TGTTTCATNN CTCAAAGAC CGTCAGACAA CATTATAGC AATGTTTCTA GGAGACACGN 240
CAACTCTACT GTCGATATTA AACCGGAGAT TCCCAGAATT GGGTTTGGTC CGGTCTGACT 300
```

GTACCGNAAC AAGCNNTTGG ATCCAATCTG TGCTATTTTT GGGACAAATA TCCCAGGTTG 360

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCTTCACTGT CACCAAAACG TTAGAACAAG ACGCAAGATT GAAGACTATT TCTAAGTGGC 60
AACAAATTTT ATCCAAGATT ATTGAAGAGA TACACATCCG AGTGGTACTC AGAGCAGCTG 120
GAAATGATGG AAACAAGACT GTGACAATGA CCTACCTAGG TCAGTTTCTT GGCGAGAAAG 180
GCACCTTGCT GAAGGTTATG GAGAAGGCTT TTCCAGAACT AGGGTTAACT CAAAAGGATT 240
GTACTGAAAT GAGCTGGATT GAAGCCGCCC TTTTCCATGG TGGRTTCCA ACAGGKTCTC 300
CTATTGAAAT TTTGCTTMAG CTCAAGTCGC CTYTAGGAAA AGRTTWCTTC AAAGCAACGK 360
CGGATTTTCGT TAAAGAACCT WTTCTGTGA TAGGGCTCAA AGGAATATTC AAAAGATTGA 420
TTGAAGG 427

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
GTTGTACTAT CATNGAAGAT TAAGTTAGTC GATGTTCCGT CCACGGTCAC CGNGTTTAAA 60
GTCCAGAAAC ATNAGGAGAA AGAGGCCGTT AGGNTCATCA ACAAGTGGCA GTATGTTGCG 120
GATAAGGTCC CTGAAGATCT TTTCATCAGC GCAACGTTGG NGAGATCAAA CGGAAACTCT 180
GTGCAGGCTT TGTTTACTGG ACTCTATCTT GGNCCGGTGA ATAATNTCTT GGCCTTGATG 240
GAAGAAAAGT TTCCAGANTT AGGTCTTGAT ATCCAAGNCT GCACAGAGAT GAGTTGGGCT 300
GAATCTGCAC TCTGGTNTNC TGNTTTCNCT AAAGGAGAGN CTCCTTGGGT GTTCNCGCG 360
GATCGGNAGC GGNCAATTTN TGGNCTTTCA AGGGGAAAGN CGGCTTTTNN CAAGAACCCG 420
NTACCCGGGG TTCAATT 437
```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
GCGGACCCTA TAGATCANNA TGTGCTACTG ANAGAAGAGG AAGCCAAGAA CAAGCCGGAG 60
```

ACAGATAAAT ATCTGAAATG GGNCGATANC GTTTACGAAT TTATGACNCC ATATGTTTCG 120
 AAATCTCCAA GAGGAGCTTA TGTCAATTTC AAGGATATGG ATTTGGGTAT GTATCTTGGA 180
 AAGAAGAAGA CAAAGTACGA GGAAGGAAAG AGTTGGGGAG TGAAGTATTT CAAGAACAAT 240
 TTCGAGAGAT TGGTGAGAGT GAAGACTAGG GTTGATCCAA CAGATTTCTT CTGCGATGAA 300
 CAGAGCATTCT CTCTGGTGAA CAAAGTTACC TGAAGATATC ATTTGAAGTT TTTTATTAGT 360
 CCCTTTTCTC TGTGAAATCA TCTGTGCGTG TTGAATATTA TCGTCAAGT GTGTAACCTA 420
 TGTGTGTGAT TGTGAATTGT G 441

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGGCTTAAC ACAACGTCGT TTTGGGCCAA TTACCCGGCG GGTACACCCA AGAGCATCCT 60
 TCTAGATAGG CCTCCGACGA ATTCAGTGTC ATTTAAGAGT AAATCGGATT TTGTCAAAAA 120
 ACCAATACCC AAAAAAGGTT TAGAGAAGCT TTGGAAGACA ATGTTTAAAT TCAACAGTAG 180
 CGTCTCGTTG CAATTCAACC CTTACGGTGG AGTGATGGAC CGGATTCCGG CAACGGCCAC 240
 CGCTTTTCCT CATCGGAAAG GAAACTTGTT CAAGGTTCAA TACNCTACGA TGTGGTTTGA 300
 CGCAAACGCC ACACAGAGTA GCCNGGCTAT GATGAATGAG CTTTTTGAGG TGGCGGGACC 360
 GTACGTGNGT CAAGTAAACC CGAGANANGG CTTCTTTTAA NTTTCAGAGNC CATCGNTNTT 420
 NGGAGCAANN CCAAGTGGGG GGGNCCAACC GGGGGNTNAA ANCNNAGNTC TTNGGGGGCC 480

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
NGGGAATTGC NCGAGGNAAG TTGTACCCAA TTCCTGGACC ACCATTGGTT TCCCAAGAA 60
CCCGAGACAA CCGTTTTTCA ATNACCGTGA TGTTGATTG GGTATTAATT CTCATAATGG 120
TAAAATCAGT AGTTATGTGG AAGGTAAACG TTACGGGAAG AAGTATTTTCG CAGGTAATTT 180
CGAGAGATTG GTGAAGATTA AGACGAGAGT TGATAGTGGT AATTTCTTTA GGAACGAACA 240
GAGTATTCCT GTGTTACCAT AAGTGTATTT ATTTGATTAT TGGTTAGTGA AATTTGTTGT 300
TGTATAATGA TTATATGTCG TATTTTTATT TATTATTAGT AATTTATAAA GTTTGATATT 360
AAATACAAAT AGTATAATAA GATAGTTTCT TTTAGTAAAA 400
```

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
CAACTCTAAT GGGAACACCT ACTTCGATCG AATGTCGATG GGGGAAGAGC TTTTCTGGGC 60
GGTTCGAGGA GGTGGAGCCG CGAGTTTCGG CATCGTGATG GGATACAAAA TCCGGTTGGT 120
TCCGGTTCCG GAGAAAGTTA CGGTTTTTAG CGTCGGAAAA ACCGTCGGAG AAGGAGCCGT 180
TGATCTTATA ATGAAGTGGC AGAACTTCTC TCATAGTACG GNTCGGAATT TTTTTGTGAA 240
GCTGANTTTT GANTTTAGTC AACGGTGCAA AGCCGGGTGA AAAAAAGGTT TTAGNGNCTT 300
TCANTTTGGN TGNAANCTTG GGGGTTTTAT NAGAACGGTT AACCGGGATT NANCCCGNGT 360
TTTCCCGGGG TAAAACCTT NGG 383
```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
ATCAATGTTT TACTAAACG TACACGAGCA TCGTTGGCTT TCAAGGCTAA ATCTGATTTT 60
NTTCAAGAAC CGATNCCTAA AACCGCGATT TCGAAGCTTT GGAGACGGTT GCAAGAACCG 120
```

GAAGCAGAGC ATGCTCAGCT AATTTNCACN CCATTTGGTG GTAAAATGAG TNAGATTGCA 180
 GATTACGAAA CACCATTTC GCATAGGAAG GGGAAATATAT ATNAGATTCA GTACTTGAAT 240
 TACTGGAGAG GAGACGTGAA AGAGAAGTAT ATTGAGATNG GTGGAGGAGA GTTTACGGTT 300
 GNTATNAGTA AGTTTTTTGG CGAAGTNTNC CNAGAGGNGN CTTNNTNTAA ACCT 354

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTTTTTAGTA CACTAATAAT CAAATGGAAT GAGAAATGAA GCCACAAAAG TATCTGCAAT 60
 CAAAATATCC TGCTATCTCC ATCTCAAGCT CTCAATAGTA TCCTCTCCGA AAGTGAAATC 120
 AACATTTCAA ACTCTATTTT TTGGTGGAAT CGATAGACTG ATTCCTCTGA TGAACCAGAA 180
 GTTTCCGGAA CTCGGCTTAC GATCTCAAGA CTGTTCCGGAA ATGAGCTGGA TCGAATCGAT 240
 AATGTTCTTC AACTGGAGAT CAGGACAGCC GTTAGAGATT TTGCTCAACA GAGACCTAAG 300
 GATTCGAGGA TCAGTATTTT AAAGCAAAGT CAGGATTATG GTTCAAAAAC CCGTTCCTGA 360
 AAACGTTTTT CGAAGAGGTA TCCAAGGGGT TTCTCGAGCA AGT 403

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
GAGATGAGTT GGATTAANTC TGTACTCTGG TTTGCTGATT TCCCTAAAGG AGAATCTCTT  60
NGTGTCTCA CGAATCGTAA GCGTACATCT CTATCTTTNA AAGGCAAAGA TGATTTTATC 120
CAAGAACCGA TACCCGAGGC TGCAATTNAA GAGATATGGA GGCGATTAGA AGCCCCCNAG 180
GCTCGGCTTG GAAAGATCAT ATTA ACTCCA TTTGGTGGGA AAATNAGTGA AATGGCAGAG 240
TACGTANCAC CATTCCCACA                                     260
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
CTCTTGCATA TTCGCTGCAA GGATGGGAAA TTCAAACCA CTCCCTACAA TTTTTGTAT  60
```

TATAGTTTCA GTCTTGTATT TTTAATTCTA TTGCATAACA CCAACTTCTT CATCAGCCTC 120
CATCCAAGAT CAATTCATAA ACTGTGTCAA AAGAAACACA CATGTTTCTT TTCCACTCGA 180
GAAAACGTTA TTCACCCCTG CGAAAAACGT CTCTTTGTTC AACCAAGTCC TTGANTCGAC 240
GGCTCAAAAT CTCCAGTTCT TGGCAAAATC CATGCCTAAA CCGGGRTTCA TATTCAGACC 300
GATTCACCAG TCTCAAGTCC AAGSTTCCAT CATTTGTTCA AMGRAACTCG GGNTTCATTT 360
TNGTGTTTGA NGTGGCGGTC ACGATTTTCG AGGCCTTTGT NTTTATGTTT CACGGTTTGA 420
AAAAACCGTT TATATTACTC GGCCTGTCAA ANTTGNANNC AAAATCANAT GTTGGATATT 480
GNATTCCAAA TAGGTNCTTG GGGTNAACCT GGTGGCTANC GTTTGGTGAG CTTTTACTTT 540
CAAGAATTTG CANGNGGANG TGCAAAGATT CCATGGGATT TCCCGGGGGG TTTNTTGCAC 600
AATGT 605

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AACACAAAAC TCTTCCATTT GGCTTCTCTC TTGCATATTC GTTGCAAGGA TGGGAAATTC 60
AAAACCACTC CCTACAATTN CTTGTATTAT CGTTTCAGTC TTGTATTTTN NATTCCTATTG 120
CATAACACCA ACTTCTTCAT CAGCCTCCAT CCAAGNTCAA TTCATAAACT GTGTCAAAAG 180
GAACACACAT GTTTCTTTTC CACTCGAGNA AACGGTATTC ACTCCTGCGG AAAACGGCTC 240
TNTTATTCAA CGGGTCCNTG AATCGACGGG TCAAAATCTC CAGTTCTTGG NAAAATCCAT 300

GNCTAAACCG GGGTTCATAT TCAGGCCGGT TCACCAGTCT CAAGTCCAAG NTTCCATCAT 360
 TTGTTCAAAG GAACTCGGGA TTCATTTCCG CGNTAGAAAGT GGCGGGCANN GGTTTCGGGG 420
 CCTGTCTNTT GNTTANGGGN AGGAAAACCG GTTNTATTNC TCGG 464

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCGGGAGCCC ANGNTAAATT ANNTGAAAAT GGGGNCGNAT ANCCGTTTAC NGAATTTTAT 60
 GACNCCCAAT ATGTTTCGAA ATCTCAAAGA NNGGGANCTT ATGTCAATTT CAAGGATATG 120
 GATTTGGGTA TGTATCTTGG AAAGNAGAAG ACAAAGTACG AGGAAGGAAA GAGTTGGGGA 180
 GTGAAGTATT TCAAGAACAA TTTCGAGAGA TTGGTGAGAG TGAAGACTAG GGTTGATCCN 240
 ACAGATTTTCN TCTGCGATGA ACAGAGCATT CCTCTGGTGN ACAAAGTTAC CTGAAGATAT 300
 CATTTGAAGT TTTTATTAG TCCCTTTTCT CTGTGAAATC ATCTGTGCGT GTTGAATANT 360
 ATGCGTCAAG TGTGTAAC TT ATGTGT 386

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
TACCATAGGG AGGTGGTGNA AGATTTTGTA TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60
TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120
TTCATTGAAG CTAAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180
AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCCACCT 240
ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300
ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCTG CAATGTGGAC ACTACTCTAA 360
ATAAAATGTC ATTTACC 377
```

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

TACCATAGGG AGGTGGTGNA AGATTTTGTA TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60
 TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120
 TTCATTGAAG CTAAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180
 AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCCACCT 240
 ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300
 ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCTG CAATGTGGAC ACTACTCTAA 360
 ATAAAATGTC ATTTACC 377

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..346
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAGCTGTGGA TATGGTCACA AATGGCAATC GGTGGTCCG AAAACTGATC CGAATCTTTT 60
 TATGAGAATN TTGATTCAAC CAGTGACGAG GAAGAAGGTA AAGACTGTGA GAGCTTCTNT 120
 GGTGCCCCTN TTTTNAGGCN AGACAGATGA AGTTTTTGCT TTCCTTAGTA AGGAGTTTCC 180
 TGAATTGGGT TTAAAGAAGG AGAATTNTTC GGAGATGACT TGGTTTCANT CTGCTTTATG 240
 GTGGGACAAT CGTCTTAATG CTAATCAGGT TGATCCTAAA GTNTTTCTTG ATCGGAATCT 300
 CGATACCTCG AGTTTCGGTA AGAGGAAATC GGATTACGTC GCGACT 346

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ATGGGGTGAG ACTTATTTCA AAGGTAATTT CAAGAGATTA GGTTCGGTTA AAGGGAAGNT 60
TGATCCAACA AATTTCTTCA GGAACGAACA GAGTATTCCT CCTCTGTTTT GAGTCCTCAA 120
TACAAAACCA GATATAAAG ATGTCATTTT ATTTTTTCAA TTATAATAGA TAATGTAAGT 180
TTCTGCTACA ATTGTAAAAG TGAGATGTAC CCAATACGGT TTAAGCGGAC CGAGAATAGT 240
CAATTCAAAG ACCAAATTCT G 261
```

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCTCAAAGGA CTAACCATGA AAACCTCCTC AAGTGTCTCT CTCACCGANT CAACGAGGAC 60
GACTCAAGAN TTATACACAC ATCAAAAGAT CCTTCGTATT TNTCAATCTT GATTTCTTCC 120
ATACAAAATC CAAGTTTCTC TGTTCTCGAA ACACCTAAAC CGGTTTCAAT CATCACTCCG 180
GTTCAAGCCA CCGATGTTCA ATCTACGNTT AAATNCGCAC GGNCTTCACG GGTATACACA 240
ATCAGGGCTA GGAGTGGTNG TCATGACTAC GGAGGTTTAT CTTTACATTG GCTTAAAAAN 300
CANNCCGTTT GTTNNTCATT GATTTNNAGA AATCTTCCGG GCTTATTTAA CATNTAAGAT 360
GTTTGATAAN CCGGNNCCNG TTTGGGGTTC AAATCCCGGT GGCTTACAAA NTTNGGGGGA 420
ATTGTNCCTA TGAGGTTTGG AAAATTAANG CAAAATNTTT TGGGCCTTCC CGGCCGGT 478

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGCCGTTAGG ATCATCAAGA AATGGCAATA TGCTGCAGAT AAGGTCCTG ATGATCTTTT 60
CATTAGGACA ACATTGGAGA GATCAAACAA GAACGCAGTA CACGCTTGT TCACTGGACT 120
ATATATTGGT CCGGTGAACA ATCTATTGGC GTTGATGGAA GAAAAGTTTC CGGAACTAGG 180
TCTTGAGAAA GAAGGTTGTG AAGAGATGAG TTGGATTGAG TCTGTACTCT GGTTCGCTGA 240
TTTCCCTAAA GGAGAATCTC TTGGTGTCT CACGAATCGT GAGCGTACAT CTCTATCTTT 300
CAAAGGCAAA GATGATTTTG TCCAAGAACC GATACCCGAG GCTGCAATTC AAGAGATATG 360

GAGGCGATTA GAAGCCCCCG AGGCTCGGCT TGGAAAGATC ATATTAACTC CATTGGGTG 420
 NGGNAAAATG AGTGAAATGG CAGAGNCCGA ACCACCAATT CCCACANNCG AGGGAGGGGA 480
 ACCCCTNTGN GGNTCAGAAT GTGGTTCCTG GNNNNNAAGN GGGNGCCAGN ACCAANCCGG 540
 GNCNGTAAAN CNTGNAATGG GCCNAACCCG TNCCGGATT 579

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Oryza sativa*
- (B) STRAIN: Nipponbare, subsp. japonica
- (D) DEVELOPMENTAL STAGE: etiolated shoot (8 days old)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGTCCTGGAA GGTCCGCCTC GTGCAGGTTN CGACGACGGT GACGGTGTTT CTCGTCGGGA 60
 GGAACGTCGA CCAGGGCGCC GCNGACGTCG TCGCCAGATG GCAAGACGTC GCGCCGAGCC 120
 TCCCTCCCGA GCTCACCATA CGGGTGATCG TNCGAGGGCA GCGCGCCACG TTCCAGTCGC 180
 TGTACCTCGG CTCGTGCGCC GACCTGGTGC CGACGATGAG CAGCATGTTC CCGGAGCTCG 240
 GGATGACGAT TG 252

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /label= Ambiguous
/note= "Xaa = Cys or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20..21
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa-Xaa probably is Ser-Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Xaa Leu Asn Asn Arg
1           5           10           15
Ala Asp Pro Xaa Xaa
           20
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa = probably Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /label= ambiguous
 /note= "Xaa = probably Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /label= ambiguous
 /note= "Xaa = probably Trp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /label= ambiguous
 /note= "Xaa = probably Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Xaa Ile Xaa Val Xaa Ile Glu Asp Glu Thr Ala Xaa Val Gln Ala Gly
1 5 10 15
Ala Thr Leu Gly Glu Val Tyr Xaa
20

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lactuca sativa
 (B) STRAIN: lollo bionda

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Tyr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ACTTCTACTT CTATTATTGA TAGGTTTACT CA

32

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactuca sativa*
(B) STRAIN: lollo bionda

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACT	TCT	ACT	TCT	ATT	ATT	GAT	AGG	TTT	ACT	CAA	TGT	CTA	AAC	AAC	CGA	48
Thr	Ser	Thr	Ser	Ile	Ile	Asp	Arg	Phe	Thr	Gln	Cys	Leu	Asn	Asn	Arg	
1				5				10						15		
GCT	GAC	CCT	TCT	TTC	CCG	CTC	AGT	GGA	CAA	CTT	TAC	ACT	CCC	GAT	AAC	96
Ala	Asp	Pro	Ser	Phe	Pro	Leu	Ser	Gly	Gln	Leu	Tyr	Thr	Pro	Asp	Asn	
			20					25						30		
TCC	TCT	TTT	CCA	TCC	GTC	TTG	CAA	GCT	TAC	ATC	CGG	AAC	CTC	CGA	TTC	144
Ser	Ser	Phe	Pro	Ser	Val	Leu	Gln	Ala	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	
		35					40						45			
AAT	GAA	TCC	ACG	ACT	CCC	AAA	CCC	ATC	TTA	ATC	ATC	ACC	GCC	TTA	CAC	192
Asn	Glu	Ser	Thr	Thr	Pro	Lys	Pro	Ile	Leu	Ile	Ile	Thr	Ala	Leu	His	
	50					55				60						
CCT	TCA	CAC	ATT	CAA	GCA	GCT	GTT	GTG	TGC	GCC	AAA	ACA	CAC	CGC	CTG	240
Pro	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Ala	Lys	Thr	His	Arg	Leu	

65	70	75	80	
CTA ATG AAA ACC AGA AGC GGA GGC CAT GAT TAT GAG GGG CTT TCC TAT				288
Leu Met Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr				
	85	90	95	
GTG ACC AAT TCG AAC CAA CCC TTT TTT GTT GTT GAC ATG TTC AAC TTA				336
Val Thr Asn Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu				
	100	105	110	
CGC TCC ATA AAC GTG AGT ATT GAA GAT GAA ACT GCA TGG GTC CAA GCC				384
Arg Ser Ile Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala				
	115	120	125	
GGC GCC ACC CTC GGA GAA GTT				405
Gly Ala Thr Leu Gly Glu Val				
	130	135		

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg				
1	5	10	15	
Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn				
	20	25	30	
Ser Ser Phe Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe				
	35	40	45	
Asn Glu Ser Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His				
	50	55	60	
Pro Ser His Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu				
	65	70	75	80
Leu Met Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr				
	85	90	95	
Val Thr Asn Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu				
	100	105	110	
Arg Ser Ile Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala				
	115	120	125	

Gly Ala Thr Leu Gly Glu Val
130 135

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CACGTTTATG GAGCGTAAGT TGAAC

25

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CACCCTTCAC ACATTCAAGC AGC

23

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1981 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactuca sativa

(B) STRAIN: lollo bionda

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..1626

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(372, "g")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(379, "g")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(786, "t")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(1105..1106, "ga")

(D) OTHER INFORMATION: /note= "also possible "gg" and "aa"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACAAAA	ATG	GCA	ATT	ACC	TAT	TCT	TTC	AAC	TTC	AAA	TCT	TAT	ATT	TTT	48	
	Met	Ala	Ile	Thr	Tyr	Ser	Phe	Asn	Phe	Lys	Ser	Tyr	Ile	Phe		
	1				5					10						
CCT	CTC	CTC	CTT	GTC	TTG	CTC	TCT	ACC	CAT	TCA	TCA	GCG	ACT	TCA	ACT	96
Pro	Leu	Leu	Leu	Val	Leu	Leu	Ser	Thr	His	Ser	Ser	Ala	Thr	Ser	Thr	
15					20					25					30	
TCC	ATT	ATA	GAT	CGC	TTC	ACC	CAA	TGT	CTA	AAC	AAC	CGA	GCT	GAC	CCT	144
Ser	Ile	Ile	Asp	Arg	Phe	Thr	Gln	Cys	Leu	Asn	Asn	Arg	Ala	Asp	Pro	
				35					40					45		
TCT	TTC	CCG	CTC	AGT	GGA	CAA	CTT	TAC	ACT	CCC	GAT	AAC	TCC	TCT	TTT	192
Ser	Phe	Pro	Leu	Ser	Gly	Gln	Leu	Tyr	Thr	Pro	Asp	Asn	Ser	Ser	Phe	
			50					55					60			
CCA	TCC	GTC	TTG	CAA	GCT	TAC	ATC	CGG	AAC	CTC	CGA	TTC	AAT	GAA	TCC	240
Pro	Ser	Val	Leu	Gln	Ala	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	Asn	Glu	Ser	
		65					70					75				
ACG	ACT	CCC	AAA	CCC	ATC	TTA	ATC	ATC	ACC	GCC	TTA	CAC	CCT	TCA	CAC	288
Thr	Thr	Pro	Lys	Pro	Ile	Leu	Ile	Ile	Thr	Ala	Leu	His	Pro	Ser	His	
		80				85					90					
ATT	CAA	GCA	GCT	GTT	GTG	TGC	GCC	AAA	ACA	CAC	CGC	CTG	CTA	ATG	AAA	336
Ile	Gln	Ala	Ala	Val	Val	Cys	Ala	Lys	Thr	His	Arg	Leu	Leu	Met	Lys	
95					100					105					110	
ACC	AGA	AGC	GGA	GGC	CAT	GAT	TAT	GAG	GGG	CTT	TCC	TAT	GTG	ACC	AAT	384

Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Val	Thr	Asn	
			115						120					125		
TCG	AAC	CAA	CCC	TTT	TTT	GTT	GTT	GAC	ATG	TTC	AAC	TTA	CGC	TCC	ATA	432
Ser	Asn	Gln	Pro	Phe	Phe	Val	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	
			130					135					140			
AAC	GTG	AGT	ATT	GAA	GAT	GAA	ACT	GCA	TGG	GTC	CAA	GCT	GGT	GCG	ACT	480
Asn	Val	Ser	Ile	Glu	Asp	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	
		145					150					155				
CTT	GGT	GAA	GTC	TAC	TAC	CGA	ATA	GCA	GAG	AAA	AGC	AAC	AGT	CAT	GCT	528
Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Ser	His	Ala	
	160					165					170					
TTT	CCG	GCT	GGC	GTT	TGC	CCT	ACT	GTT	GGA	GTT	GGT	GGC	CAT	TTT	AGT	576
Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	
175					180				185						190	
GGT	GGT	GGT	TAT	GGT	AAC	TTG	ATG	GGA	AAA	TAC	GGC	CTT	TCT	GTT	GAC	624
Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Gly	Lys	Tyr	Gly	Leu	Ser	Val	Asp	
				195				200					205			
AAT	ATT	GTC	GAT	GCT	CAG	TTA	ATC	GAT	GTG	AAT	GGT	AAA	CTT	CTG	AAT	672
Asn	Ile	Val	Asp	Ala	Gln	Leu	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asn	
			210					215					220			
CGG	AAA	TCA	ATG	GGT	GAA	GAT	CTT	TTT	TGG	GCC	ATC	ACA	GGT	GGT	GGT	720
Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Thr	Gly	Gly	Gly	
		225					230					235				
GGT	GTC	AGC	TTT	GGT	GTG	GTT	GTA	GCG	TAC	AAG	ATC	AAA	CTG	GTT	CGT	768
Gly	Val	Ser	Phe	Gly	Val	Val	Val	Ala	Tyr	Lys	Ile	Lys	Leu	Val	Arg	
	240					245					250					
GTT	CCT	ACC	ACT	GTG	ACC	GTT	TTT	AAC	GTA	CAA	AGA	ACA	TCC	GAG	CAG	816
Val	Pro	Thr	Thr	Val	Thr	Val	Phe	Asn	Val	Gln	Arg	Thr	Ser	Glu	Gln	
255					260				265					270		
AAC	CTA	AGC	ACC	ATA	GCC	CAC	CGA	TGG	ATA	CAA	GTT	GCG	GAT	AAG	CTC	864
Asn	Leu	Ser	Thr	Ile	Ala	His	Arg	Trp	Ile	Gln	Val	Ala	Asp	Lys	Leu	
				275				280						285		
GAT	AAT	GAC	CTT	TTC	CTT	CGA	ATG	ACC	TTT	AAC	GTG	ATA	AAC	AAC	ACA	912
Asp	Asn	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	Asn	Val	Ile	Asn	Asn	Thr	
			290				295					300				
AAT	GGC	GAA	AAG	ACG	ATA	CGT	GGT	TTG	TTT	CCA	ACA	CTG	TAC	CTC	GGA	960
Asn	Gly	Glu	Lys	Thr	Ile	Arg	Gly	Leu	Phe	Pro	Thr	Leu	Tyr	Leu	Gly	
		305					310					315				
AAC	TCT	ACC	GCT	CTT	GTT	GCC	CTC	CTG	AAC	AAG	GAT	TTC	CCT	GAA	TTA	1008
Asn	Ser	Thr	Ala	Leu	Val	Ala	Leu	Leu	Asn	Lys	Asp	Phe	Pro	Glu	Leu	
	320					325					330					

GGT	GTA	GAA	ATT	TCA	GAT	TGT	ATT	GAA	ATG	AGT	TGG	ATC	GAG	TCT	GTT	1056
Gly	Val	Glu	Ile	Ser	Asp	Cys	Ile	Glu	Met	Ser	Trp	Ile	Glu	Ser	Val	
335					340					345					350	
CTT	TTC	TAC	ACA	AAC	TTC	CCC	ATT	GGT	ACT	CCG	ACC	ACT	GCT	CTT	CTA	1104
Leu	Phe	Tyr	Thr	Asn	Phe	Pro	Ile	Gly	Thr	Pro	Thr	Thr	Ala	Leu	Leu	
				355					360					365		
AGC	CGT	ACA	CCT	CAA	AGA	CTA	AAC	CCA	TTC	AAA	ATC	AAA	TCT	GAT	TAC	1152
Ser	Arg	Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	Lys	Ile	Lys	Ser	Asp	Tyr	
			370					375					380			
GTA	AAA	AAC	ACT	ATT	TCC	AAA	CAG	GGA	TTC	GAA	TCC	ATA	TTT	GAA	AGG	1200
Val	Lys	Asn	Thr	Ile	Ser	Lys	Gln	Gly	Phe	Glu	Ser	Ile	Phe	Glu	Arg	
		385					390					395				
ATG	AAA	GAA	CTC	GAA	AAC	CAA	ATG	CTA	GCT	TTC	AAC	CCT	TAT	GGT	GGA	1248
Met	Lys	Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	Phe	Asn	Pro	Tyr	Gly	Gly	
	400					405					410					
AGA	ATG	AGC	GAA	ATT	TCC	GAA	TTT	GCA	AAG	CCT	TTT	CCC	CAT	CGA	TCA	1296
Arg	Met	Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	Pro	Phe	Pro	His	Arg	Ser	
415					420					425					430	
GGG	AAT	ATA	GCG	AAG	ATC	CAA	TAC	GAA	GTA	AAC	TGG	GAT	GAA	CTT	GGC	1344
Gly	Asn	Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	Asn	Trp	Asp	Glu	Leu	Gly	
				435					440					445		
GTT	GAA	GCA	GCC	AAT	CGG	TAC	TTG	AAC	TTC	ACA	AGG	GTG	ATG	TAT	GAT	1392
Val	Glu	Ala	Ala	Asn	Arg	Tyr	Leu	Asn	Phe	Thr	Arg	Val	Met	Tyr	Asp	
			450					455					460			
TAT	ATG	ACT	CCG	TTT	GTT	TCT	AAG	AAC	CCC	AGG	GAA	GCA	TTT	CTG	AAC	1440
Tyr	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Glu	Ala	Phe	Leu	Asn	
		465					470					475				
TAC	AGG	GAT	TTA	GAT	ATT	GGT	GTC	AAC	AGT	CAT	GGC	AAG	AAT	GCT	TAC	1488
Tyr	Arg	Asp	Leu	Asp	Ile	Gly	Val	Asn	Ser	His	Gly	Lys	Asn	Ala	Tyr	
	480					485					490					
GGT	GAA	GGA	ATG	GTT	TAT	GGG	CAC	AAG	TAT	TTC	AAA	GAG	ACG	AAT	TAT	1536
Gly	Glu	Gly	Met	Val	Tyr	Gly	His	Lys	Tyr	Phe	Lys	Glu	Thr	Asn	Tyr	
495					500					505					510	
AAG	AGG	CTA	ACG	ATG	GTG	AAG	ACG	AGG	GTT	GAT	CCT	AGC	AAT	TTT	TTT	1584
Lys	Arg	Leu	Thr	Met	Val	Lys	Thr	Arg	Val	Asp	Pro	Ser	Asn	Phe	Phe	
				515					520					525		
AGG	AAT	GAG	CAA	AGT	ATC	CCA	ACT	TTG	TCA	TCT	TCA	TGG	AAG			1626
Arg	Asn	Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser	Ser	Ser	Trp	Lys			
			530					535				540				
TAAATTCTAA ATTCACCTTGT GAAATTGAAT AAAAGTATGG CTTTTTCAAG GTCATGGTAT																1686

CCAGATTCAG ATGATATTGA TATAATTTTG ACTTGTATTT ATACAAACAA AATTATATTA 1746
TATTTTCTG AATTTAGATT TTCCATTCTT TGGAAAAATA TACGAACATT GATGTTGATA 1806
TTTTTAAGAA TTATAGATTT TGAACATTGT GAACAATGAA TAAACCGAGG ACTTCCCTTG 1866
GGTTTTTTTT ATAAGTATGT AATAGCATGT CTTTAATCAA GATAACCGAT CATTGGATGC 1926
AATTTATTAT TATAAACCTT ATTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA 1981

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Met	Ala	Ile	Thr	Tyr	Ser	Phe	Asn	Phe	Lys	Ser	Tyr	Ile	Phe	Pro	Leu	1	5	10	15
Leu	Leu	Val	Leu	Leu	Ser	Thr	His	Ser	Ser	Ala	Thr	Ser	Thr	Ser	Ile	20	25	30	
Ile	Asp	Arg	Phe	Thr	Gln	Cys	Leu	Asn	Asn	Arg	Ala	Asp	Pro	Ser	Phe	35	40	45	
Pro	Leu	Ser	Gly	Gln	Leu	Tyr	Thr	Pro	Asp	Asn	Ser	Ser	Phe	Pro	Ser	50	55	60	
Val	Leu	Gln	Ala	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	Asn	Glu	Ser	Thr	Thr	65	70	75	80
Pro	Lys	Pro	Ile	Leu	Ile	Ile	Thr	Ala	Leu	His	Pro	Ser	His	Ile	Gln	85	90	95	
Ala	Ala	Val	Val	Cys	Ala	Lys	Thr	His	Arg	Leu	Leu	Met	Lys	Thr	Arg	100	105	110	
Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Val	Thr	Asn	Ser	Asn	115	120	125	
Gln	Pro	Phe	Phe	Val	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	130	135	140	
Ser	Ile	Glu	Asp	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	145	150	155	160
Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Ser	His	Ala	Phe	Pro	165	170	175	

Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	Gly	Gly		
			180					185					190				
Gly	Tyr	Gly	Asn	Leu	Met	Gly	Lys	Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile		
		195					200					205					
Val	Asp	Ala	Gln	Leu	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asn	Arg	Lys		
	210					215					220						
Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val		
225					230					235					240		
Ser	Phe	Gly	Val	Val	Val	Ala	Tyr	Lys	Ile	Lys	Leu	Val	Arg	Val	Pro		
			245						250					255			
Thr	Thr	Val	Thr	Val	Phe	Asn	Val	Gln	Arg	Thr	Ser	Glu	Gln	Asn	Leu		
		260						265					270				
Ser	Thr	Ile	Ala	His	Arg	Trp	Ile	Gln	Val	Ala	Asp	Lys	Leu	Asp	Asn		
	275						280					285					
Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	Asn	Val	Ile	Asn	Asn	Thr	Asn	Gly		
	290					295					300						
Glu	Lys	Thr	Ile	Arg	Gly	Leu	Phe	Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser		
305					310					315					320		
Thr	Ala	Leu	Val	Ala	Leu	Leu	Asn	Lys	Asp	Phe	Pro	Glu	Leu	Gly	Val		
			325						330					335			
Glu	Ile	Ser	Asp	Cys	Ile	Glu	Met	Ser	Trp	Ile	Glu	Ser	Val	Leu	Phe		
		340						345					350				
Tyr	Thr	Asn	Phe	Pro	Ile	Gly	Thr	Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg		
		355					360					365					
Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	Lys	Ile	Lys	Ser	Asp	Tyr	Val	Lys		
	370					375					380						
Asn	Thr	Ile	Ser	Lys	Gln	Gly	Phe	Glu	Ser	Ile	Phe	Glu	Arg	Met	Lys		
385					390					395					400		
Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met		
			405						410					415			
Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	Pro	Phe	Pro	His	Arg	Ser	Gly	Asn		
		420						425					430				
Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	Asn	Trp	Asp	Glu	Leu	Gly	Val	Glu		
	435						440					445					
Ala	Ala	Asn	Arg	Tyr	Leu	Asn	Phe	Thr	Arg	Val	Met	Tyr	Asp	Tyr	Met		
	450					455					460						

Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Glu	Ala	Phe	Leu	Asn	Tyr	Arg
465					470					475				480	
Asp	Leu	Asp	Ile	Gly	Val	Asn	Ser	His	Gly	Lys	Asn	Ala	Tyr	Gly	Glu
				485					490					495	
Gly	Met	Val	Tyr	Gly	His	Lys	Tyr	Phe	Lys	Glu	Thr	Asn	Tyr	Lys	Arg
			500					505						510	
Leu	Thr	Met	Val	Lys	Thr	Arg	Val	Asp	Pro	Ser	Asn	Phe	Phe	Arg	Asn
		515					520					525			
Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser	Ser	Ser	Trp	Lys				
530						535					540				

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTAATGATC TCCTTTCTTG TTTGACC

27

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGAGCGGCCG CTATATTACA ACTTCTCCAC CATCACTCCT C

41

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GGTGATGTTA ATGATAATCT CCTC

24

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

AGAGCGGCCG CTACAATTCC TTCAACATGT AAATTCCTC

40

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACTTCCCGTA GAAACTCGGA GACTTTCACA CAATGC

36

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TCCATCCAAG ATCAATTCAT AAACGTGTGC

30

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGAGCGGCCG CTTTCATGAA CCTAGCTTCT AGTAGG

36

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAGCGGCCG CGAAATGGCC CCCCTTTTAA AACGGGG

37

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGAGCGGCCG CAAATGATAT CTTCAGGTAA CTTTGTTTAC

40

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGAGCGGCCG CATAATCAAA TAAATACACT TATGGTAACA CAG

43

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGAGCGGCCG CTGGTTTTGT ATTGAGGACT CAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1757 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: Colombia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1..570, 801..1754)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ACT	TCC	CGT	AGA	AAC	TCG	GAG	ACT	TTC	ACA	CAA	TGC	CTA	ACC	TCA	AAC	48
Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	
1				5					10					15		
TCC	GAC	CCC	AAA	CAT	CCC	ATC	TCC	CCC	GCT	ATC	TTC	TTC	TCC	GGA	AAT	96
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	
			20					25					30			
GGC	TCC	TAC	TCC	TCC	GTA	TTA	CAA	GCC	AAC	ATC	CGT	AAC	CTC	CGC	TTC	144
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	
		35				40						45				
AAC	ACC	ACC	TCA	ACT	CCG	AAA	CCC	TTC	CTC	ATA	ATC	GCC	GCA	ACA	CAT	192
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	
	50					55					60					
GAA	TCC	CAT	GTG	CAA	GCC	GCG	ATT	ACT	TGC	GGG	AAA	CGC	CAC	AAC	CTT	240
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
65				70					75					80		
CAG	ATG	AAA	ATC	AGA	AGT	GGA	GGC	CAC	GAC	TAC	GAT	GGC	TTG	TCA	TAC	288
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	
			85					90					95			
GTT	ACA	TAC	TCT	GGC	AAA	CCG	TTC	TTC	GTC	CTC	GAC	ATG	TTT	AAC	CTC	336
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	
		100					105						110			
CGT	TCG	GTG	GAT	GTC	GAT	GTG	GCA	AGT	AAG	ACC	GCG	TGG	GTC	CAA	ACC	384
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	
		115					120					125				
GGT	GCC	ATA	CTC	GGA	GAA	GTT	TAT	TAC	TAT	ATA	TGG	GAG	AAG	AGC	AAA	432
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	
	130					135					140					
ACC	CTA	GCT	TAT	CCC	GCC	GGA	ATT	TGT	CCC	ACG	GTT	GGT	GTC	GGT	GGC	480
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	
145					150				155						160	
CAT	ATC	AGT	GGT	GGA	GGT	TAC	GGT	AAC	ATG	ATG	AGA	AAA	TAC	GGT	CTC	528
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	

165	170	175	
ACC GTA GAT AAT ACC ATC GAT GCA AGA ATG GTC GAC GTT AAT			570
Thr Val Asp Asn Thr Ile Asp Ala Arg Met Val Asp Val Asn			
180	185	190	
GGTATAATTG ATATCTCTAT TTTATATACT AATTAAATTT TATAGTGTGG ATCGGATAGT			630
GATTTTGGTC CATCAATTAA AAAC TTGGTG AACATAAAAT TAACCAAGCA ATCAATTTAG			690
ACAAGCAACA TAATCATATA TATTTTCTT ACATTTGTAT GTACCTGAAT ATTTATATTT			750
ATGTTTATAT GTTCTCACTA TATTTTCACT TTTGTATTTG AAAATTTTGA GGA AAA			806
			Gly Lys
ATT TTG GAT AGA AAA TTG ATG GGA GAA GAT CTC TAC TGG GCA ATA AAC			854
Ile Leu Asp Arg Lys Leu Met Gly Glu Asp Leu Tyr Trp Ala Ile Asn			
195	200	205	
GGA GGA GGA GGA GGG AGC TAC GGC GTC GTA TTG GCC TAC AAA ATA AAC			902
Gly Gly Gly Gly Gly Ser Tyr Gly Val Val Leu Ala Tyr Lys Ile Asn			
210	215	220	
CTT GTT GAA GTC CCA GAA AAC GTC ACC GTT TTC AGA ATC TCC CGG ACG			950
Leu Val Glu Val Pro Glu Asn Val Thr Val Phe Arg Ile Ser Arg Thr			
225	230	235	240
TTA GAA CAA AAT GCG ACG GAT ATC ATT CAC CGG TGG CAA CAA GTT GCA			998
Leu Glu Gln Asn Ala Thr Asp Ile Ile His Arg Trp Gln Gln Val Ala			
245	250	255	
CCG AAG CTT CCC GAC GAG CTT TTC ATA AGA ACA GTC ATT GAC GTA GTA			1046
Pro Lys Leu Pro Asp Glu Leu Phe Ile Arg Thr Val Ile Asp Val Val			
260	265	270	
AAC GGC ACT GTT TCA TCT CAA AAG ACC GTC AGG ACA ACA TTC ATA GCA			1094
Asn Gly Thr Val Ser Ser Gln Lys Thr Val Arg Thr Thr Phe Ile Ala			
275	280	285	
ATG TTT CTA GGA GAC ACG ACA ACT CTA CTG TCG ATA TTA AAC CGG AGA			1142
Met Phe Leu Gly Asp Thr Thr Thr Leu Leu Ser Ile Leu Asn Arg Arg			
290	295	300	
TTC CCA GAA TTG GGT TTG GTC CGG TCT GAC TGT ACC GAA ACA AGC TGG			1190
Phe Pro Glu Leu Gly Leu Val Arg Ser Asp Cys Thr Glu Thr Ser Trp			
305	310	315	320
ATC CAA TCT GTG CTA TTC TGG ACA AAT ATC CAA GTT GGT TCG TCG GAG			1238
Ile Gln Ser Val Leu Phe Trp Thr Asn Ile Gln Val Gly Ser Ser Glu			
325	330	335	
ACA CTT CTA CTC CAA AGG AAT CAA CCC GTG AAC TAC CTC AAG AGG AAA			1286
Thr Leu Leu Leu Gln Arg Asn Gln Pro Val Asn Tyr Leu Lys Arg Lys			
340	345	350	

TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1334
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
		355					360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1382
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
		370				375					380					
TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TTA	CGG	GTG	ACT	CCG	TTC	CCA	1430
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Leu	Arg	Val	Thr	Pro	Phe	Pro	
					390					395					400	
TAC	AGA	GCC	GGT	AAT	CTC	TGG	AAG	ATT	CAG	TAC	GGT	GCG	AAT	TGG	AGA	1478
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg	
				405					410					415		
GAT	GAG	ACT	TTA	ACC	GAC	CGG	TAC	ATG	GAA	TTG	ACG	AGG	AAG	TTG	TAC	1526
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr	
			420					425					430			
CAA	TTC	ATG	ACA	CCA	TTT	GTT	TCC	AAG	AAT	CCG	AGA	CAA	TCG	TTT	TTC	1574
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe	
		435					440					445				
AAT	AAC	CGT	GAT	GTT	GAT	TTG	GGT	ATT	AAT	TCT	CAT	AAT	GGT	AAA	ATC	1622
Asn	Asn	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile	
		450				455					460					
AGT	AGT	TAT	GTG	GAA	GGT	AAA	CGT	TAC	GGG	AAG	AAG	TAT	TTC	GCA	GGT	1670
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly	
					470				475						480	
AAT	TTC	GAG	AGA	TTG	GTG	AAG	ATT	AAG	ACG	AGA	GTT	GAT	AGT	GGT	AAT	1718
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn	
				485					490					495		
TTC	TTT	AGG	AAC	GAA	CAC	AGT	ATT	CCT	GTG	TTA	CCA	TAA				1757
Phe	Phe	Arg	Asn	Glu	His	Ser	Ile	Pro	Val	Leu	Pro					
			500					505								

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn
1				5					10					15	

Ser Asp Pro Lys His Pro Ile Ser Pro Ala Ile Phe Phe Ser Gly Asn
 20 25 30
 Gly Ser Tyr Ser Ser Val Leu Gln Ala Asn Ile Arg Asn Leu Arg Phe
 35 40 45
 Asn Thr Thr Ser Thr Pro Lys Pro Phe Leu Ile Ile Ala Ala Thr His
 50 55 60
 Glu Ser His Val Gln Ala Ala Ile Thr Cys Gly Lys Arg His Asn Leu
 65 70 75 80
 Gln Met Lys Ile Arg Ser Gly Gly His Asp Tyr Asp Gly Leu Ser Tyr
 85 90 95
 Val Thr Tyr Ser Gly Lys Pro Phe Phe Val Leu Asp Met Phe Asn Leu
 100 105 110
 Arg Ser Val Asp Val Asp Val Ala Ser Lys Thr Ala Trp Val Gln Thr
 115 120 125
 Gly Ala Ile Leu Gly Glu Val Tyr Tyr Tyr Ile Trp Glu Lys Ser Lys
 130 135 140
 Thr Leu Ala Tyr Pro Ala Gly Ile Cys Pro Thr Val Gly Val Gly Gly
 145 150 155 160
 His Ile Ser Gly Gly Gly Tyr Gly Asn Met Met Arg Lys Tyr Gly Leu
 165 170 175
 Thr Val Asp Asn Thr Ile Asp Ala Arg Met Val Asp Val Asn Gly Lys
 180 185 190
 Ile Leu Asp Arg Lys Leu Met Gly Glu Asp Leu Tyr Trp Ala Ile Asn
 195 200 205
 Gly Gly Gly Gly Gly Ser Tyr Gly Val Val Leu Ala Tyr Lys Ile Asn
 210 215 220
 Leu Val Glu Val Pro Glu Asn Val Thr Val Phe Arg Ile Ser Arg Thr
 225 230 235 240
 Leu Glu Gln Asn Ala Thr Asp Ile Ile His Arg Trp Gln Gln Val Ala
 245 250 255
 Pro Lys Leu Pro Asp Glu Leu Phe Ile Arg Thr Val Ile Asp Val Val
 260 265 270
 Asn Gly Thr Val Ser Ser Gln Lys Thr Val Arg Thr Thr Phe Ile Ala
 275 280 285
 Met Phe Leu Gly Asp Thr Thr Thr Leu Leu Ser Ile Leu Asn Arg Arg
 290 295 300

Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	305	310	315	320
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	325	330	335	
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	340	345	350	
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	355	360	365	
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	370	375	380	
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Leu	Arg	Val	Thr	Pro	Phe	Pro	385	390	395	400
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg	405	410	415	
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr	420	425	430	
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe	435	440	445	
Asn	Asn	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile	450	455	460	
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly	465	470	475	480
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn	485	490	495	
Phe	Phe	Arg	Asn	Glu	His	Ser	Ile	Pro	Val	Leu	Pro					500	505		

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: Colombia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACT	TCC	CGT	AGA	AAC	TCG	GAG	ACT	TTC	ACA	CAA	TGC	CTA	ACC	TCA	AAC	48
Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	
1				5				10						15		
TCC	GAC	CCC	AAA	CAT	CCC	ATC	TCC	CCC	GCT	ATC	TTC	TTC	TCC	GGA	AAT	96
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	
			20					25					30			
GGC	TCC	TAC	TCC	TCC	GTA	TTA	CAA	GCC	AAC	ATC	CGT	AAC	CTC	CGC	TTC	144
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	
			35				40					45				
AAC	ACC	ACC	TCA	ACT	CCG	AAA	CCC	TTC	CTC	ATA	ATC	GCC	GCA	ACA	CAT	192
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	
			50			55					60					
GAA	TCC	CAT	GTG	CAA	GCC	GCG	ATT	ACT	TGC	GGG	AAA	CGC	CAC	AAC	CTT	240
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
	65				70				75					80		
CAG	ATG	AAA	ATC	AGA	AGT	GGA	GGC	CAC	GAC	TAC	GAT	GGC	TTG	TCA	TAC	288
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	
				85				90					95			
GTT	ACA	TAC	TCT	GGC	AAA	CCG	TTC	TTC	GTC	CTC	GAC	ATG	TTT	AAC	CTC	336
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	
			100					105					110			
CGT	TCG	GTG	GAT	GTC	GAC	GTG	GCA	AGT	AAG	ACC	GCG	TGG	GTC	CAA	ACC	384
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	
		115					120					125				
GGT	GCC	ATA	CTC	GGA	GAA	GTT	TAT	TAC	TAT	ATA	TGG	GAG	AAG	AGC	AAA	432
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	
	130					135					140					
ACC	CTA	GCT	TAT	CCC	GCC	GGA	ATT	TGT	CCC	ACG	GTT	GGT	GTC	GGT	GGC	480
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	
	145				150				155						160	
CAT	ATC	AGT	GGT	GGA	GGT	TAC	GGT	AAC	ATG	ATG	AGA	AAA	TAC	GGT	CTC	528
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	
			165					170						175		

ACC	GTA	GAT	AAT	ACC	ATC	GAT	GCA	AGA	ATG	GTC	GAC	GTA	AAT	GGA	AAA	576
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	
			180					185					190			
ATT	TTG	GAT	AGA	AAA	TTG	ATG	GGA	GAA	GAT	CTC	TAC	TGG	GCA	ATA	AAC	624
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	
		195					200				205					
GGA	GGA	GGA	GGA	GGG	AGC	TAC	GGC	GTC	GTA	TTG	GCC	TAC	AAA	ATA	AAC	672
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	
	210					215					220					
CTT	GTT	GAA	GTC	CCA	GAA	AAC	GTC	ACC	GTT	TTC	AGA	ATC	TCC	CGG	ACG	720
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	
225					230				235						240	
TTA	GAA	CAA	AAT	GCG	ACG	GAT	ATC	ATT	CAC	CGG	TGG	CAA	CAA	GTT	GCA	768
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	
				245				250					255			
CCG	AAG	CTT	CCC	GAC	GAG	CTT	TTC	ATA	AGA	ACA	GTC	ATT	GAC	GTA	GTA	816
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	
			260					265					270			
AAC	GGC	ACT	GTT	TCA	TCT	CAA	AAG	ACC	GTC	AGG	ACA	ACA	TTC	ATA	GCA	864
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	
		275					280					285				
ATG	TTT	CTA	GGA	GAC	ACG	ACA	ACT	CTA	CTG	TCG	ATA	TTA	AAC	CGG	AGA	912
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	
	290					295				300						
TTC	CCA	GAA	TTG	GGT	TTG	GTC	CGG	TCT	GAC	TGT	ACC	GAA	ACA	AGC	TGG	960
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	
305					310					315					320	
ATC	CAA	TCT	GTG	CTA	TTC	TGG	ACA	AAT	ATC	CAA	GTT	GGT	TCG	TCG	GAG	1008
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	
				325				330					335			
ACA	CTT	CTA	CTC	CAA	AGG	AAT	CAA	CCC	GTG	AAC	TAC	CTC	AAG	AGG	AAA	1056
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	
			340					345					350			
TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1104
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
		355					360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1152
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
	370					375					380					
TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TCT	ACG	GTG	ACT	CCG	TTC	CCA	1200
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Ser	Thr	Val	Thr	Pro	Phe	Pro	

385	390	395	400	
TAC AGA GCC GGT AAT CTC TGG AAG ATT CAG TAC GGT GCG AAT TGG AGA	1248			
Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg				
405	410	415		
GAT GAG ACT TTA ACC GAC CGG TAC ATG GAA TTG ACG AGG AAG TTG TAC	1296			
Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr				
420	425	430		
CAA TTC ATG ACA CCA TTT GTT TCC AAG AAT CCG AGA CAA TCG TTT TTC	1344			
Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe				
435	440	445		
AAT TAC CGT GAT GTT GAT TTG GGT ATT AAT TCT CAT AAT GGT AAA ATC	1392			
Asn Tyr Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile				
450	455	460		
AGT AGT TAT GTG GAA GGT AAA CGT TAC GGG AAG AAG TAT TTC GCA GGT	1440			
Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly				
465	470	475	480	
AAT TTC GAG AGA TTG GTG AAG ATT AAG ACG AGA GTT GAT AGT GGT AAT	1488			
Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn				
485	490	495		
TTC TTT AGG AAC GAA CAG AGT ATT CCT GTG TTA CCA TAA	1527			
Phe Phe Arg Asn Glu Gln Ser Ile Pro Val Leu Pro				
500	505			

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Thr Ser Arg Arg Asn Ser Glu Thr Phe Thr Gln Cys Leu Thr Ser Asn	
1 5 10 15	
Ser Asp Pro Lys His Pro Ile Ser Pro Ala Ile Phe Phe Ser Gly Asn	
20 25 30	
Gly Ser Tyr Ser Ser Val Leu Gln Ala Asn Ile Arg Asn Leu Arg Phe	
35 40 45	
Asn Thr Thr Ser Thr Pro Lys Pro Phe Leu Ile Ile Ala Ala Thr His	
50 55 60	

Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	65	70	75	80
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	85	90	95	
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	100	105	110	
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	115	120	125	
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	130	135	140	
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	145	150	155	160
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	165	170	175	
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	180	185	190	
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	195	200	205	
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	210	215	220	
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	225	230	235	240
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	245	250	255	
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	260	265	270	
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	275	280	285	
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	290	295	300	
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	305	310	315	320
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	325	330	335	
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	340	345	350	

Ser Asp Tyr Val Arg Glu Pro Ile Ser Arg Thr Gly Leu Glu Ser Ile
 355 360 365
 Trp Lys Lys Met Ile Glu Leu Glu Ile Pro Thr Met Ala Phe Asn Pro
 370 375 380
 Tyr Gly Gly Glu Met Gly Arg Ile Ser Ser Thr Val Thr Pro Phe Pro
 385 390 395 400
 Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg
 405 410 415
 Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr
 420 425 430
 Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe
 435 440 445
 Asn Tyr Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile
 450 455 460
 Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly
 465 470 475 480
 Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn
 485 490 495
 Phe Phe Arg Asn Glu Gln Ser Ile Pro Val Leu Pro
 500 505

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: Colombia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCC	ATC	CAA	GAT	CAA	TTC	ATA	AAC	TGT	GTC	AAA	AGA	AAC	ACA	CAT	GTT	48
Ser	Ile	Gln	Asp	Gln	Phe	Ile	Asn	Cys	Val	Lys	Arg	Asn	Thr	His	Val	
1				5					10					15		
TCT	TTT	CCA	CTC	GAG	AAA	ACG	TTA	TTC	ACC	CCT	GCG	AAA	AAC	GTC	TCT	96
Ser	Phe	Pro	Leu	Glu	Lys	Thr	Leu	Phe	Thr	Pro	Ala	Lys	Asn	Val	Ser	
			20					25					30			
TTG	TTC	AAC	CAA	GTC	CTT	GAA	TCG	ACG	GCT	CAA	AAT	CTC	CAG	TTC	TTG	144
Leu	Phe	Asn	Gln	Val	Leu	Glu	Ser	Thr	Ala	Gln	Asn	Leu	Gln	Phe	Leu	
		35					40					45				
GCA	AAA	TCC	ATG	CCT	AAA	CCG	GGA	TTC	ATA	TTC	AGA	CCG	ATT	CAC	CAG	192
Ala	Lys	Ser	Met	Pro	Lys	Pro	Gly	Phe	Ile	Phe	Arg	Pro	Ile	His	Gln	
	50					55					60					
TCT	CAA	GTC	CAA	GCT	TCC	ATC	ATT	TGT	TCA	AAG	AAA	CTC	GGA	ATT	CAT	240
Ser	Gln	Val	Gln	Ala	Ser	Ile	Ile	Cys	Ser	Lys	Lys	Leu	Gly	Ile	His	
65					70				75						80	
TTT	CGT	GTT	AGA	AGT	GGC	GGT	CAC	GAT	TTC	GAG	GCC	TTG	TCT	TAT	GTT	288
Phe	Arg	Val	Arg	Ser	Gly	Gly	His	Asp	Phe	Glu	Ala	Leu	Ser	Tyr	Val	
				85					90					95		
TCA	CGG	ATT	GAA	AAA	CCG	TTT	ATA	TTA	CTC	GAC	CTG	TCA	AAA	TTG	AAA	336
Ser	Arg	Ile	Glu	Lys	Pro	Phe	Ile	Leu	Leu	Asp	Leu	Ser	Lys	Leu	Lys	
			100					105					110			
CAA	ATC	AAT	GTT	GAT	ATT	GAA	TCC	AAT	AGT	GCT	TGG	GTT	CAA	CCT	GGT	384
Gln	Ile	Asn	Val	Asp	Ile	Glu	Ser	Asn	Ser	Ala	Trp	Val	Gln	Pro	Gly	
		115					120					125				
GCT	ACG	CTT	GGT	GAG	CTT	TAC	TAC	AGA	ATT	GCA	GAG	AAG	AGC	AAG	ATC	432
Ala	Thr	Leu	Gly	Glu	Leu	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Lys	Ile	
	130					135					140					
CAT	GGA	TTT	CCC	GCG	GGT	TTG	TGC	ACA	AGT	GTA	GGC	ATA	GGT	GGG	TAT	480
His	Gly	Phe	Pro	Ala	Gly	Leu	Cys	Thr	Ser	Val	Gly	Ile	Gly	Gly	Tyr	
145					150					155					160	
ATG	ACA	GGC	GGT	GGA	TAC	GGT	ACC	TTG	ATG	AGG	AAG	TAT	GGT	CTT	GCG	528
Met	Thr	Gly	Gly	Gly	Tyr	Gly	Thr	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ala	
				165				170						175		
GGA	GAT	AAT	GTT	CTA	GAC	GTA	AAG	ATG	GTT	GAT	GCA	AAT	GGT	AAA	TTA	576
Gly	Asp	Asn	Val	Leu	Asp	Val	Lys	Met	Val	Asp	Ala	Asn	Gly	Lys	Leu	
			180				185						190			
CTC	GAC	AGA	GCC	GCG	ATG	GGT	GAG	GAC	CTA	TTT	TGG	GCG	ATT	AGA	GGA	624
Leu	Asp	Arg	Ala	Ala	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Arg	Gly	
		195					200					205				

GGC	GGT	GGA	GCG	AGT	TTC	GGG	ATA	GTT	CTA	GCA	TGG	AAG	ATC	AAG	CTT	672
Gly	Gly	Gly	Ala	Ser	Phe	Gly	Ile	Val	Leu	Ala	Trp	Lys	Ile	Lys	Leu	
	210					215					220					
GTT	CCT	GTT	CCT	AAG	ACT	GTT	ACC	GTC	TTC	ACT	GTC	ACC	AAA	ACG	TTA	720
Val	Pro	Val	Pro	Lys	Thr	Val	Thr	Val	Phe	Thr	Val	Thr	Lys	Thr	Leu	
225					230					235					240	
GAA	CAA	GAC	GCA	AGA	TTG	AAG	ACT	ATT	TCT	AAG	TGG	CAA	CAA	ATT	TCA	768
Glu	Gln	Asp	Ala	Arg	Leu	Lys	Thr	Ile	Ser	Lys	Trp	Gln	Gln	Ile	Ser	
				245					250					255		
TCC	AAG	ATT	ATT	GAA	GAG	ATA	CAC	ATC	CGA	GTG	GTA	CTC	AGA	GCA	GCT	816
Ser	Lys	Ile	Ile	Glu	Glu	Ile	His	Ile	Arg	Val	Val	Leu	Arg	Ala	Ala	
			260					265					270			
GGA	AAT	GAT	GGA	AAC	AAG	ACT	GTG	ACA	ATG	ACC	TAC	CTA	GGT	CAG	TTT	864
Gly	Asn	Asp	Gly	Asn	Lys	Thr	Val	Thr	Met	Thr	Tyr	Leu	Gly	Gln	Phe	
		275					280					285				
CTT	GGC	GAG	AAA	GGC	ACC	TTG	CTG	AAG	GTT	ATG	GAG	AAG	GCT	TTT	CCA	912
Leu	Gly	Glu	Lys	Gly	Thr	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Phe	Pro	
	290					295					300					
GAA	CTA	GGG	TTA	ACT	CAA	AAG	GAT	TGT	ACT	GAA	ATG	AGC	TGG	ATT	GAA	960
Glu	Leu	Gly	Leu	Thr	Gln	Lys	Asp	Cys	Thr	Glu	Met	Ser	Trp	Ile	Glu	
305					310					315					320	
GCC	GCC	CTT	TTC	CAT	GGT	GGA	TTT	CCA	ACA	GGT	TCT	CCT	ATT	GAA	ATT	1008
Ala	Ala	Leu	Phe	His	Gly	Gly	Phe	Pro	Thr	Gly	Ser	Pro	Ile	Glu	Ile	
				325				330					335			
TTG	CTT	CAG	CTC	AAG	TCG	CCT	CTA	GGA	AAA	GAT	TAC	TTC	AAA	GCA	ACG	1056
Leu	Leu	Gln	Leu	Lys	Ser	Pro	Leu	Gly	Lys	Asp	Tyr	Phe	Lys	Ala	Thr	
			340					345					350			
TCG	GAT	TTC	GTT	AAA	GAA	CCT	ATT	CCT	GTG	ATA	GGC	TTC	AAA	GGA	ATA	1104
Ser	Asp	Phe	Val	Lys	Glu	Pro	Ile	Pro	Val	Ile	Gly	Phe	Lys	Gly	Ile	
		355					360					365				
TTC	AAA	AGA	TTG	ATT	GAA	GGA	AAC	ACA	ACA	TTT	CTG	AAC	TGG	ACT	CCT	1152
Phe	Lys	Arg	Leu	Ile	Glu	Gly	Asn	Thr	Thr	Phe	Leu	Asn	Trp	Thr	Pro	
	370					375					380					
TAC	GGT	GGT	ATG	ATG	TCG	AAA	ATC	CCT	GAA	TCT	GCG	ATC	CCA	TTT	CCG	1200
Tyr	Gly	Gly	Met	Met	Ser	Lys	Ile	Pro	Glu	Ser	Ala	Ile	Pro	Phe	Pro	
385					390				395						400	
CAT	AGA	AAC	GGA	ACC	CTC	TTC	AAG	ATT	CTC	TAT	TAC	GCG	AAC	TGG	CTA	1248
His	Arg	Asn	Gly	Thr	Leu	Phe	Lys	Ile	Leu	Tyr	Tyr	Ala	Asn	Trp	Leu	
				405					410					415		

GAG AAT GAC AAG ACA TCG AGT AGA AAA ATC AAC TGG ATC AAA GAG ATA	1296
Glu Asn Asp Lys Thr Ser Ser Arg Lys Ile Asn Trp Ile Lys Glu Ile	
420 425 430	
TAC AAT TAC ATG GCG CCT TAT GTC TCA AGC AAT CCA AGA CAA GCA TAT	1344
Tyr Asn Tyr Met Ala Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr	
435 440 445	
GTG AAC TAC AGA GAT CTA GAC TTC GGA CAG AAC AAG AAC AAC GCA AAG	1392
Val Asn Tyr Arg Asp Leu Asp Phe Gly Gln Asn Lys Asn Asn Ala Lys	
450 455 460	
GTT AAC TTC ATT GAA GCT AAA ATC TGG GGA CCT AAG TAC TTC AAA GGC	1440
Val Asn Phe Ile Glu Ala Lys Ile Trp Gly Pro Lys Tyr Phe Lys Gly	
465 470 475 480	
AAT TTT GAC AGA TTG GTG AAG ATT AAA ACC AAG GTT GAT CCA GAG AAC	1488
Asn Phe Asp Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn	
485 490 495	
TTC TTC AGG CAC GAG CAG AGT ATC CCA CCT ATG CCC TAC TAG	1530
Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr	
500 505	

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ser Ile Gln Asp Gln Phe Ile Asn Cys Val Lys Arg Asn Thr His Val	
1 5 10 15	
Ser Phe Pro Leu Glu Lys Thr Leu Phe Thr Pro Ala Lys Asn Val Ser	
20 25 30	
Leu Phe Asn Gln Val Leu Glu Ser Thr Ala Gln Asn Leu Gln Phe Leu	
35 40 45	
Ala Lys Ser Met Pro Lys Pro Gly Phe Ile Phe Arg Pro Ile His Gln	
50 55 60	
Ser Gln Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Gly Ile His	
65 70 75 80	
Phe Arg Val Arg Ser Gly Gly His Asp Phe Glu Ala Leu Ser Tyr Val	
85 90 95	
Ser Arg Ile Glu Lys Pro Phe Ile Leu Leu Asp Leu Ser Lys Leu Lys	

100					105					110						
Gln	Ile	Asn	Val	Asp	Ile	Glu	Ser	Asn	Ser	Ala	Trp	Val	Gln	Pro	Gly	
115					120					125						
Ala	Thr	Leu	Gly	Glu	Leu	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Lys	Ile	
130					135					140						
His	Gly	Phe	Pro	Ala	Gly	Leu	Cys	Thr	Ser	Val	Gly	Ile	Gly	Gly	Tyr	
145					150					155					160	
Met	Thr	Gly	Gly	Gly	Tyr	Gly	Thr	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ala	
165					170					175						
Gly	Asp	Asn	Val	Leu	Asp	Val	Lys	Met	Val	Asp	Ala	Asn	Gly	Lys	Leu	
180					185					190						
Leu	Asp	Arg	Ala	Ala	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Arg	Gly	
195					200					205						
Gly	Gly	Gly	Ala	Ser	Phe	Gly	Ile	Val	Leu	Ala	Trp	Lys	Ile	Lys	Leu	
210					215					220						
Val	Pro	Val	Pro	Lys	Thr	Val	Thr	Val	Phe	Thr	Val	Thr	Lys	Thr	Leu	
225					230					235					240	
Glu	Gln	Asp	Ala	Arg	Leu	Lys	Thr	Ile	Ser	Lys	Trp	Gln	Gln	Ile	Ser	
245					250					255						
Ser	Lys	Ile	Ile	Glu	Glu	Ile	His	Ile	Arg	Val	Val	Leu	Arg	Ala	Ala	
260					265					270						
Gly	Asn	Asp	Gly	Asn	Lys	Thr	Val	Thr	Met	Thr	Tyr	Leu	Gly	Gln	Phe	
275					280					285						
Leu	Gly	Glu	Lys	Gly	Thr	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Phe	Pro	
290					295					300						
Glu	Leu	Gly	Leu	Thr	Gln	Lys	Asp	Cys	Thr	Glu	Met	Ser	Trp	Ile	Glu	
305					310					315					320	
Ala	Ala	Leu	Phe	His	Gly	Gly	Phe	Pro	Thr	Gly	Ser	Pro	Ile	Glu	Ile	
325					330					335						
Leu	Leu	Gln	Leu	Lys	Ser	Pro	Leu	Gly	Lys	Asp	Tyr	Phe	Lys	Ala	Thr	
340					345					350						
Ser	Asp	Phe	Val	Lys	Glu	Pro	Ile	Pro	Val	Ile	Gly	Phe	Lys	Gly	Ile	
355					360					365						
Phe	Lys	Arg	Leu	Ile	Glu	Gly	Asn	Thr	Thr	Phe	Leu	Asn	Trp	Thr	Pro	
370					375					380						
Tyr	Gly	Gly	Met	Met	Ser	Lys	Ile	Pro	Glu	Ser	Ala	Ile	Pro	Phe	Pro	

385		390		395		400
His Arg Asn Gly Thr Leu Phe Lys Ile Leu Tyr Tyr Ala Asn Trp Leu						
	405			410		415
Glu Asn Asp Lys Thr Ser Ser Arg Lys Ile Asn Trp Ile Lys Glu Ile						
	420			425		430
Tyr Asn Tyr Met Ala Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr						
	435			440		445
Val Asn Tyr Arg Asp Leu Asp Phe Gly Gln Asn Lys Asn Asn Ala Lys						
	450			455		460
Val Asn Phe Ile Glu Ala Lys Ile Trp Gly Pro Lys Tyr Phe Lys Gly						
	465			470		475
Asn Phe Asp Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn						
	485			490		495
Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr						
	500			505		

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met Glu Asn Lys Thr Pro Ile Phe Phe Ser Leu Ser Ile Phe Leu Ser			
1	5	10	15
Leu Leu Asn Cys Ala Leu Gly Gly Asn Asp Leu Leu Ser Cys Leu Thr			
	20	25	30
Phe Asn Gly Val Arg Asn His Thr Val Phe Ser Ala Asp Ser Asp Ser			
	35	40	45
Asp Phe Asn Arg Phe Leu His Leu Ser Ile Gln Asn Pro Leu Phe Gln			
	50	55	60
Asn Ser Leu Ile Ser Lys Pro Ser Ala Ile Ile Leu Pro Gly Ser Lys			
	65	70	75
			80

Glu Glu Leu Ser Asn Thr Ile Arg Cys Ile Arg Lys Gly Ser Trp Thr
85 90 95

Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr
100 105 110

Ser Asp Thr Pro Phe Ile Leu Ile Asp Leu Met Asn Leu Asn Arg Val
115 120 125

Ser Ile Asp Leu Glu Ser Glu Thr Ala Trp Val Glu Ser Gly Ser Thr
130 135 140

Leu Gly Glu Leu Tyr Tyr Ala Ile Thr Glu Ser Ser Ser Lys Leu Gly
145 150 155 160

Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Thr Gly Gly His Ile Ser
165 170 175

Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp
180 185 190

Asn Val Val Asp Ala Ile Leu Ile Asp Ala Asn Gly Ala Ile Leu Asp
195 200 205

Arg Gln Ala Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
210 215 220

Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro
225 230 235 240

Val Pro Glu Lys Val Thr Val Phe Arg Val Thr Lys Asn Val Ala Ile
245 250 255

Asp Glu Ala Thr Ser Leu Leu His Lys Trp Gln Phe Val Ala Glu Glu
260 265 270

Leu Glu Glu Asp Phe Thr Leu Ser Val Leu Gly Gly Ala Asp Glu Lys
275 280 285

Gln Val Trp Leu Thr Met Leu Gly Phe His Phe Gly Leu Lys Thr Val
290 295 300

Ala Lys Ser Thr Phe Asp Leu Leu Phe Pro Glu Leu Gly Leu Val Glu
305 310 315 320

Glu Asp Tyr Leu Glu Met Ser Trp Gly Glu Ser Phe Ala Tyr Leu Ala
325 330 335

Gly Leu Glu Thr Val Ser Gln Leu Asn Asn Arg Phe Leu Lys Phe Asp
340 345 350

Glu Arg Ala Phe Lys Thr Lys Val Asp Leu Thr Lys Glu Pro Leu Pro
355 360 365

Ser Lys Ala Phe Tyr Gly Gly Leu Leu Glu Arg Leu Ser Lys Glu Pro
370 375 380

Asn Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Gln Met Ser Lys Ile
385 390 395 400

Ser Ser Asp Phe Thr Pro Phe Pro His Arg Ser Gly Thr Arg Leu Met
405 410 415

Val Glu Tyr Ile Val Ala Trp Asn Gln Ser Glu Gln Lys Lys Lys Thr
420 425 430

Glu Phe Leu Asp Trp Leu Glu Lys Val Tyr Glu Phe Met Lys Pro Phe
435 440 445

Val Ser Lys Asn Pro Arg Leu Gly Tyr Val Asn His Ile Asp Leu Asp
450 455 460

Leu Gly Gly Ile Asp Trp Gly Asn Lys Thr Val Val Asn Asn Ala Ile
465 470 475 480

Glu Ile Ser Arg Ser Trp Gly Glu Ser Tyr Phe Leu Ser Asn Tyr Glu
485 490 495

Arg Leu Ile Arg Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn
500 505 510

His Pro Gln Ser Ile Pro Pro Met Ala Asn Phe Asp Tyr Leu Glu Lys

515

520

525

Thr Leu Gly Ser Asp Gly Gly Glu Val Val Ile
 530 535

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met Met Cys Arg Ser Leu Thr Leu Arg Phe Phe Leu Phe Ile Val Leu
 1 5 10 15

Leu Gln Thr Cys Val Arg Gly Gly Asp Val Asn Asp Asn Leu Leu Ser
 20 25 30

Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr
 35 40 45

Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn
 50 55 60

Pro Leu Phe Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met
 65 70 75 80

Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg
 85 90 95

Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly
 100 105 110

Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn
 115 120 125

Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu

130		135		140	
Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr					
145		150		155	160
Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly					
	165		170		175
Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly					
	180		185		190
Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly					
	195		200		205
Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile					
	210		215		220
Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile					
225		230		235	240
Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys					
	245		250		255
Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr					
	260		265		270
Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly					
	275		280		285
Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly					
	290		295		300
Arg Lys Asp Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu					
305		310		315	320
Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met					
	325		330		335
Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe					
	340		345		350

Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys
355 360 365

Val Ser Val Pro Leu Asn Val Phe Arg His His Ala Leu Glu Met Leu
370 375 380

Ser Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys
385 390 395 400

Met Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly
405 410 415

Thr Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu
420 425 430

Ser Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr
435 440 445

Leu Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His
450 455 460

Ile Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr
465 470 475 480

Thr Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser
485 490 495

Ser Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn
500 505 510

Asn Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu
515 520 525

Glu Ile Tyr Met Leu Lys Glu Leu
530 535

REMARKS

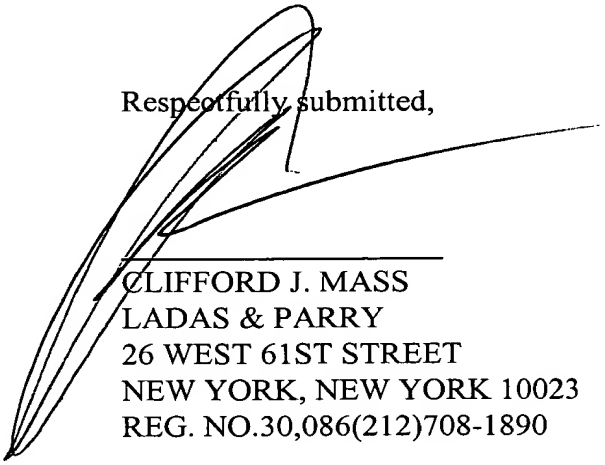
The Official Action of July 15, 2003 has been carefully considered and reconsideration of the application in view of the present submission is respectfully requested.

The indication that claims 51-53, 55, 59 and 60 are allowed has been noted with appreciation. To remove the basis for the objection to the specification, Applicants have amended the specification to include in the Sequence Listing SEQ ID NOS: 76 and 77, which correspond to the respective sequences of the berberine bridge enzymes EcBBE and PsBBE shown in Fig. 10 of the drawings. Applicants respectfully note that the present application claims the benefit of a parent PCT application which was filed prior to July 1, 1998 and that the revised sequence may thus comply with the sequence rules then in effect (see MPEP Section 2420 and 63 FR 29634 (June 1, 1998)).

Applicants submit herewith a computer readable form copy and a paper copy of the Sequence Listing along with the requisite statements that the computer readable form copy and paper copy are the same and that they contain no new matter.

In view of the above, it is respectfully submitted that the sole remaining objection to the application has been overcome and that the application is now in allowable form. An early notice of allowance is earnestly solicited and is believed to be fully warranted.

Respectfully submitted,



CLIFFORD J. MASS
LADAS & PARRY
26 WEST 61ST STREET
NEW YORK, NEW YORK 10023
REG. NO.30,086(212)708-1890

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: STUIVER, Maarten Hendrik
CUSTERS, Jerome Humbertina Henricus Victor
SELA-BURLAGE, Marianne Beatrix
MELCHERS, Leo Sjoerd
VAN DEVENTER-TROOST, Johanna Pieternella
LAGEWEG, Wessel
PONSTEIN, Anne Silene
LAGEWEG, Wessel
PONSTEIN, Anne Silene
- (ii) TITLE OF INVENTION: ANTIFUNGAL PROTEINS, DNA CODING THEREFORE,
AND HOSTS INCORPORATING SAME.
- (iii) NUMBER OF SEQUENCES: 77
- (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: LADAS & PARRY
(B) STREET 26 WEST 61 STREET
(C) CITY NEW YORK
(D) NY
(E) USA
(F) 10023 - 7604
- (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: 3.25" Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: WINDOWS 95
(D) SOFTWARE: WORDPERFECT 8
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/258,031
 - (B) FILING DATE: 25-FEB-1999
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/EP97/04923
 - (B) FILING DATE: 04-SEP-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP97200831.2
 - (B) FILING DATE: 19-MAR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP96202466.7
 - (B) FILING DATE: 04-SEP-1996

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helianthus annuus
 - (B) STRAIN: cv. zebulon
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly
 1 5 10 15

Ala Thr Leu Gly Glu Val Tyr Tyr Arg
 20 25

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helianthus annuus
 - (B) STRAIN: cv. zebulon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Xaa Ser
 1 5 10 15

Ser Phe Pro Thr Val Leu Gln Asn Tyr
 20 25

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCTCCN AGNGTNGCNC CNGCTTGNAC CCA

33

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCNTCTT TCCCNATTAC TGGNGAGGTT TA

32

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helianthus annuus*

(B) STRAIN: cv. zebulon

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAT CCG TCT TTC CCG ATT ACT GGG GAG GTT TAC ACT CCC GGA AAC TCA	48
Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser	
1 5 10 15	
TCT TTT CCT ACC GTC TTG CAA AAC TAC ATC CGA AAC CTT CGG TTC AAT	96
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn	
20 25 30	
GAA ACT ACC ACA CCA AAA CCC TTT TTA ATC ATC ACA GCC GAA CAT GTT	144
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val	
35 40 45	
TCC CAC ATT CAG GCA GCT GTG GTT TGT GGC AAA CAA AAC CGG TTG CTA	192
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu	
50 55 60	
CTG AAA ACC AGA AGC GGT GGT CAT GAT TAT GAA GGT CTT TCC TAC CTT	240
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu	
65 70 75 80	
ACA AAC ACA AAC CAA CCC TTC TTC ATT GTG GAC ATG TTC AAT TTA AGG	288
Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg	
85 90 95	
TCC ATA AAC GTA GAT ATC GAA CAA GAA ACC GCA TGG GTC CAA GCC GGC	
336	
Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly	
100 105 110	
GCC ACC CTC GGA GAA GTT	354
Ala Thr Leu Gly Glu Val	
115	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr Pro Gly Asn Ser
1 5 10 15
Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn Leu Arg Phe Asn
20 25 30
Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr Ala Glu His Val
35 40 45
Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln Asn Arg Leu Leu
50 55 60
Leu Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Leu
65 70 75 80
Thr Asn Thr Asn Gln Pro Phe Phe Ile Val Asp Met Phe Asn Leu Arg
85 90 95
Ser Ile Asn Val Asp Ile Glu Gln Glu Thr Ala Trp Val Gln Ala Gly
100 105 110
Ala Thr Leu Gly Glu Val
115

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGCAGCTG TGGTTTGTGG C

21

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTCCACAATG AAGAAGGGTT G

21

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /function= "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACGTAGATAT CGAACAAGAA ACCGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GCTTTACTAC ACGGGCTTCC CCAG

24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTGGGGAAGC CCGTGTAGTA AAGC

24

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTACTCCAA CCACGGCGCT C

21

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CGGGAAGTTG CAGAAGATTG GGTTC

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GAGCAAGAGA AGAAGGAGAC

20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1784 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helianthus annuus

(B) STRAIN: Zebulon

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 21..1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATATCACATC TTCTTTCAAC ATG CAA ACT TCC ATT CTT ACT CTC CTT CTT

50

Met Gln Thr Ser Ile Leu Thr Leu Leu Leu																
1				5				10								
CTC	TTG	CTC	TCA	ACC	CAA	TCT	TCT	GCA	ACT	TCC	CGT	TCC	ATT	ACA	GAT	98
Leu	Leu	Leu	Ser	Thr	Gln	Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp	
15				20				25								
CGC	TTC	ATT	CAA	TGT	TTA	CAC	GAC	CGG	GCC	GAC	CCT	TCA	TTT	CCG	ATA	146
Arg	Phe	Ile	Gln	Cys	Leu	His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	
30				35				40								
ACC	GGA	GAG	GTT	TAC	ACT	CCC	GGA	AAC	TCA	TCT	TTT	CCT	ACC	GTC	TTG	194
Thr	Gly	Glu	Val	Tyr	Thr	Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	
45				50				55								
CAA	AAC	TAC	ATC	CGA	AAC	CTT	CGG	TTC	AAT	GAA	ACT	ACC	ACA	CCA	AAA	242
Gln	Asn	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	
60				65				70								
CCC	TTT	TTA	ATC	ATC	ACA	GCC	GAA	CAT	GTT	TCC	CAC	ATT	CAG	GCA	GCT	290
Pro	Phe	Leu	Ile	Ile	Thr	Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	
75				80				85				90				
GTG	GTT	TGT	GGC	AAA	CAA	AAC	CGG	TTG	CTA	CTG	AAA	ACC	AGA	AGC	GGT	338
Val	Val	Cys	Gly	Lys	Gln	Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	
95				100				105								
GGT	CAT	GAT	TAT	GAA	GGT	CTT	TCC	TAC	CTT	ACA	AAC	ACA	AAC	CAA	CCC	386
Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	
110				115				120								
TTC	TTC	ATT	GTG	GAC	ATG	TTC	AAT	TTA	AGG	TCC	ATA	AAC	GTA	GAT	ATC	434
Phe	Phe	Ile	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	
125				130				135								
GAA	CAA	GAA	ACC	GCA	TGG	GTC	CAA	GCC	GGT	GCG	ACT	CTT	GGT	GAA	GTG	482
Glu	Gln	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	
140				145				150								
TAC	TAT	CGA	ATA	GCG	GAG	AAA	AGT	AAC	AAG	CAT	GGT	TTT	CCG	GCA	GGG	530
Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	
155				160				165				170				
GTT	TGT	CCA	ACG	GTT	GGC	GTT	GGT	GGG	CAT	TTT	AGT	GGT	GGT	GGG	TAT	578
Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	
175				180				185								
GGT	AAT	TTG	ATG	AGA	AAA	TAT	GGT	TTG	TCG	GTT	GAT	AAT	ATT	GTT	GAT	626
Gly	Asn	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	
190				195				200								
GCT	CAA	ATA	ATA	GAT	GTG	AAT	GGC	AAG	CTT	TTG	GAT	CGA	AAG	AGT	ATG	674
Ala	Gln	Ile	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	
205				210				215								

GGT GAG GAT TTG TTT TGG GCG ATC ACC GGC GGT GGT GGT GTT AGT TTT	722
Gly Glu Asp Leu Phe Trp Ala Ile Thr Gly Gly Gly Gly Val Ser Phe	
220 225 230	
GGT GTG GTT CTA GCC TAC AAA ATC AAA CTA GTT CGT GTT CCG GAG GTT	770
Gly Val Val Leu Ala Tyr Lys Ile Lys Leu Val Arg Val Pro Glu Val	
235 240 245 250	
GTG ACC GTG TTT ACC ATT GAA AGA AGA GAG GAA CAA AAC CTC AGC ACC	818
Val Thr Val Phe Thr Ile Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr	
255 260 265	
ATC GCG GAA CGA TGG GTA CAA GTT GCT GAT AAG CTA GAT AGA GAT CTT	866
Ile Ala Glu Arg Trp Val Gln Val Ala Asp Lys Leu Asp Arg Asp Leu	
270 275 280	
TTC CTT CGA ATG ACC TTT AGT GTC ATA AAC GAT ACC AAC GGT GGA AAG	914
Phe Leu Arg Met Thr Phe Ser Val Ile Asn Asp Thr Asn Gly Gly Lys	
285 290 295	
ACA GTC CGT GCT ATC TTT CCA ACG TTG TAC CTT GGA AAC TCG AGG AAT	962
Thr Val Arg Ala Ile Phe Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn	
300 305 310	
CTT GTT ACA CTT TTG AAT AAA GAT TTC CCC GAG TTA GGG TTG CAA GAA	1010
Leu Val Thr Leu Leu Asn Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu	
315 320 325 330	
TCG GAT TGT ACT GAA ATG AGT TGG GTT GAG TCT GTG CTT TAC TAC ACG	1058
Ser Asp Cys Thr Glu Met Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr	
335 340 345	
GGC TTC CCC AGT GGT ACT CCA ACC ACG GCG CTC TTA AGC CGT ACT CCT	1106
Gly Phe Pro Ser Gly Thr Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro	
350 355 360	
CAA AGA CTC AAC CCA TTC AAG ATC AAA TCC GAT TAT GTG CAA AAT CCT	1154
Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro	
365 370 375	
ATT TCT AAA CGA CAG TTC GAG TTC ATC TTC GAA AGG CTG AAA GAA CTT	1202
Ile Ser Lys Arg Gln Phe Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu	
380 385 390	
GAA AAC CAA ATG TTG GCT TTC AAC CCA TAT GGT GGT AGA ATG AGT GAA	1250
Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu	
395 400 405 410	
ATA TCC GAA TTC GCA AAG CCT TTC CCA CAT AGA TCG GGT AAC ATA GCG	1298
Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser Gly Asn Ile Ala	
415 420 425	
AAA ATT CAA TAC GAA GTA AAC TGG GAG GAT CTT AGC GAT GAA GCC GAA	1346
Lys Ile Gln Tyr Glu Val Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu	

430	435	440	
AAT CGT TAC TTG AAT TTC ACA AGG CTG ATG TAT GAT TAC ATG ACC CCA			1394
Asn Arg Tyr Leu Asn Phe Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro			
445	450	455	
TTT GTG TCG AAA AAC CCT AGA AAA GCA TTT TTG AAC TAT AGG GAT TTG			1442
Phe Val Ser Lys Asn Pro Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu			
460	465	470	
GAT ATT GGT ATC AAC AGC CAT GGC AGG AAT GCT TAT ACT GAA GGA ATG			1490
Asp Ile Gly Ile Asn Ser His Gly Arg Asn Ala Tyr Thr Glu Gly Met			
475	480	485	490
GTT TAT GGG CAC AAG TAT TTC AAA GAG ACA AAT TAC AAG AGG CTA GTA			1538
Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val			
495	500	505	
AGT GTG AAG ACT AAA GTT GAT CCT GAC AAC TTC TTT AGG AAT GAG CAA			1586
Ser Val Lys Thr Lys Val Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln			
510	515	520	
AGC ATC CCA ACT TTG TCA TCT T GAAGAACGTA CATATATAAA TAAATACCTT			1638
Ser Ile Pro Thr Leu Ser Ser			
525			
TGTGCATGGT ATTTTCAGGG TGTTAAAGTG ATATTCAGAT ATTTATGATA GAATTTTGAC			1698
TTGTATTTTA TACAATCAAA ATTGTATGGT TCTCCGAATT TCTCTTTTTA ATTCTGAAAA			1758
ATACATATTA GTATTGTCAA AAAAAA			1784

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Gln	Thr	Ser	Ile	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Ser	Thr	Gln	
1				5				10					15		
Ser	Ser	Ala	Thr	Ser	Arg	Ser	Ile	Thr	Asp	Arg	Phe	Ile	Gln	Cys	Leu
		20						25					30		
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr
		35					40					45			
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn

50					55					60					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr
65					70					75					80
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln
				85					90					95	
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly
			100					105					110		
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met
		115					120					125			
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp
	130					135					140				
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu
145					150					155					160
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly
				165					170					175	
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys
			180					185					190		
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val
		195					200					205			
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp
	210					215					220				
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr
225					230					235					240
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile
				245					250					255	
Glu	Arg	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val
			260					265					270		
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe
		275					280					285			
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe
	290					295					300				
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn
305					310					315					320
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met
				325					330					335	
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr

340	345	350
Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe		
355	360	365
Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro Ile Ser Lys Arg Gln Phe		
370	375	380
Glu Phe Ile Phe Glu Arg Leu Lys Glu Leu Glu Asn Gln Met Leu Ala		
385	390	395
Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu Ile Ser Glu Phe Ala Lys		
405	410	415
Pro Phe Pro His Arg Ser Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val		
420	425	430
Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu Asn Arg Tyr Leu Asn Phe		
435	440	445
Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro		
450	455	460
Arg Lys Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser		
465	470	475
His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr		
485	490	495
Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val		
500	505	510
Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser		
515	520	525
Ser		

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGCCATGGA GACTTCCATT CTTACTC

27

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCGGATCCT CAAGATGACA AAGTTGGGAT GCT

33

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helianthus annuus
(B) STRAIN: Zebulon

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG GAG ACT TCC ATT CTT ACT CTC CTT CTT CTC TTG CTC TCA ACC CAA 48
Met Glu Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Leu Ser Thr Gln
1 5 10 15

TCT TCT GCA ACT TCC CGT TCC ATT ACA GAT CGC TTC ATT CAA TGT TTA 96
Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp Arg Phe Ile Gln Cys Leu

20										25					30					
CAC	GAC	CGG	GCC	GAC	CCT	TCA	TTT	CCG	ATA	ACC	GGA	GAG	GTT	TAC	ACT	144				
His	Asp	Arg	Ala	Asp	Pro	Ser	Phe	Pro	Ile	Thr	Gly	Glu	Val	Tyr	Thr					
35					40					45										
CCC	GGA	AAC	TCA	TCT	TTT	CCT	ACC	GTC	TTG	CAA	AAC	TAC	ATC	CGA	AAC	192				
Pro	Gly	Asn	Ser	Ser	Phe	Pro	Thr	Val	Leu	Gln	Asn	Tyr	Ile	Arg	Asn					
50					55					60										
CTT	CGG	TTC	AAT	GAA	ACT	ACC	ACA	CCA	AAA	CCC	TTT	TTA	ATC	ATC	ACA	240				
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Thr					
65					70					75					80					
GCC	GAA	CAT	GTT	TCC	CAC	ATT	CAG	GCA	GCT	GTG	GTT	TGT	GGC	AAA	CAA	288				
Ala	Glu	His	Val	Ser	His	Ile	Gln	Ala	Ala	Val	Val	Cys	Gly	Lys	Gln					
85					90					95										
AAC	CGG	TTG	CTA	CTG	AAA	ACC	AGA	AGC	GGT	GGT	CAT	GAT	TAT	GAA	GGT	336				
Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly					
100					105					110										
CTT	TCC	TAC	CTT	ACA	AAC	ACA	AAC	CAA	CCC	TTC	TTC	ATT	GTG	GAC	ATG	384				
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met					
115					120					125										
TTC	AAT	TTA	AGG	TCC	ATA	AAC	GTA	GAT	ATC	GAA	CAA	GAA	ACC	GCA	TGG	432				
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp					
130					135					140										
GTC	CAA	GCC	GGT	GCG	ACT	CTT	GGT	GAA	GTG	TAC	TAT	CGA	ATA	GCG	GAG	480				
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu					
145					150					155					160					
AAA	AGT	AAC	AAG	CAT	GGT	TTT	CCG	GCA	GGG	GTT	TGT	CCA	ACG	GTT	GGC	528				
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly					
165					170					175										
GTT	GGT	GGG	CAT	TTT	AGT	GGT	GGT	GGG	TAT	GGT	AAT	TTG	ATG	AGA	AAA	576				
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys					
180					185					190										
TAT	GGT	TTG	TCG	GTT	GAT	AAT	ATT	GTT	GAT	GCT	CAA	ATA	ATA	GAT	GTG	624				
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val					
195					200					205										
AAT	GGC	AAG	CTT	TTG	GAT	CGA	AAG	AGT	ATG	GGT	GAG	GAT	TTG	TTT	TGG	672				
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp					
210					215					220										
GCG	ATC	ACC	GGC	GGT	GGT	GGT	GTT	AGT	TTT	GGT	GTG	GTT	CTA	GCC	TAC	720				
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr					
225					230					235					240					

AAA ATC AAA CTA GTT CGT GTT CCG GAG GTT GTG ACC GTG TTT ACC ATT	768
Lys Ile Lys Leu Val Arg Val Pro Glu Val Val Thr Val Phe Thr Ile	
245 250 255	
GAA AGA AGA GAG GAA CAA AAC CTC AGC ACC ATC GCG GAA CGA TGG GTA	816
Glu Arg Arg Glu Glu Gln Asn Leu Ser Thr Ile Ala Glu Arg Trp Val	
260 265 270	
CAA GTT GCT GAT AAG CTA GAT AGA GAT CTT TTC CTT CGA ATG ACC TTT	864
Gln Val Ala Asp Lys Leu Asp Arg Asp Leu Phe Leu Arg Met Thr Phe	
275 280 285	
AGT GTC ATA AAC GAT ACC AAC GGT GGA AAG ACA GTC CGT GCT ATC TTT	912
Ser Val Ile Asn Asp Thr Asn Gly Gly Lys Thr Val Arg Ala Ile Phe	
290 295 300	
CCA ACG TTG TAC CTT GGA AAC TCG AGG AAT CTT GTT ACA CTT TTG AAT	960
Pro Thr Leu Tyr Leu Gly Asn Ser Arg Asn Leu Val Thr Leu Leu Asn	
305 310 315 320	
AAA GAT TTC CCC GAG TTA GGG TTG CAA GAA TCG GAT TGT ACT GAA ATG	1008
Lys Asp Phe Pro Glu Leu Gly Leu Gln Glu Ser Asp Cys Thr Glu Met	
325 330 335	
AGT TGG GTT GAG TCT GTG CTT TAC TAC ACG GGC TTC CCC AGT GGT ACT	1056
Ser Trp Val Glu Ser Val Leu Tyr Tyr Thr Gly Phe Pro Ser Gly Thr	
340 345 350	
CCA ACC ACG GCG CTC TTA AGC CGT ACT CCT CAA AGA CTC AAC CCA TTC	1104
Pro Thr Thr Ala Leu Leu Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe	
355 360 365	
AAG ATC AAA TCC GAT TAT GTG CAA AAT CCT ATT TCT AAA CGA CAG TTC	1152
Lys Ile Lys Ser Asp Tyr Val Gln Asn Pro Ile Ser Lys Arg Gln Phe	
370 375 380	
GAG TTC ATC TTC GAA AGG ATG AAA GAA CTT GAA AAC CAA ATG TTG GCG	1200
Glu Phe Ile Phe Glu Arg Met Lys Glu Leu Glu Asn Gln Met Leu Ala	
385 390 395 400	
TTC AAC CCA TAT GGT GGT AGA ATG AGT GAA ATA TCC GAA TTC GCA AAG	1248
Phe Asn Pro Tyr Gly Gly Arg Met Ser Glu Ile Ser Glu Phe Ala Lys	
405 410 415	
CCT TTC CCA CAT AGA TCG GGT AAC ATA GCG AAG ATT CAA TAC GAA GTA	1296
Pro Phe Pro His Arg Ser Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val	
420 425 430	
AAC TGG GAG GAT CTT AGC GAT GAA GCC GAA AAT CGT TAC TTG AAT TTC	1344
Asn Trp Glu Asp Leu Ser Asp Glu Ala Glu Asn Arg Tyr Leu Asn Phe	
435 440 445	
ACA AGG CTG ATG TAT GAT TAC ATG ACT CCA TTT GTG TCG AAA AAC CCT	1392

Thr Arg Leu Met Tyr Asp Tyr Met Thr Pro Phe Val Ser Lys Asn Pro
 450 455 460

AGA GAA GCA TTT TTG AAC TAT AGG GAT TTG GAT ATT GGT ATC AAC AGC 1440
 Arg Glu Ala Phe Leu Asn Tyr Arg Asp Leu Asp Ile Gly Ile Asn Ser
 465 470 475 480

CAT GGC AGG AAT GCT TAT ACT GAA GGA ATG GTT TAT GGG CAC AAA TAT 1488
 His Gly Arg Asn Ala Tyr Thr Glu Gly Met Val Tyr Gly His Lys Tyr
 485 490 495

TTC AAA GAG ACA AAT TAC AAG AGG CTA GTA AGT GTG AAG ACT AAA GTT 1536
 Phe Lys Glu Thr Asn Tyr Lys Arg Leu Val Ser Val Lys Thr Lys Val
 500 505 510

GAT CCT GAC AAC TTC TTT AGG AAT GAG CAA AGC ATC CCA ACT TTG TCA 1584
 Asp Pro Asp Asn Phe Phe Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser
 515 520 525

TCT TG 1589
 Ser
 530

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 529 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Glu Thr Ser Ile Leu Thr Leu Leu Leu Leu Leu Ser Thr Gln
 1 5 10 15
 Ser Ser Ala Thr Ser Arg Ser Ile Thr Asp Arg Phe Ile Gln Cys Leu
 20 25 30
 His Asp Arg Ala Asp Pro Ser Phe Pro Ile Thr Gly Glu Val Tyr Thr
 35 40 45
 Pro Gly Asn Ser Ser Phe Pro Thr Val Leu Gln Asn Tyr Ile Arg Asn
 50 55 60
 Leu Arg Phe Asn Glu Thr Thr Thr Pro Lys Pro Phe Leu Ile Ile Thr
 65 70 75 80
 Ala Glu His Val Ser His Ile Gln Ala Ala Val Val Cys Gly Lys Gln
 85 90 95

Asn	Arg	Leu	Leu	Leu	Lys	Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	100	105	110
Leu	Ser	Tyr	Leu	Thr	Asn	Thr	Asn	Gln	Pro	Phe	Phe	Ile	Val	Asp	Met	115	120	125
Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val	Asp	Ile	Glu	Gln	Glu	Thr	Ala	Trp	130	135	140
Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	145	150	155
Lys	Ser	Asn	Lys	His	Gly	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	165	170	175
Val	Gly	Gly	His	Phe	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Arg	Lys	180	185	190
Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile	Val	Asp	Ala	Gln	Ile	Ile	Asp	Val	195	200	205
Asn	Gly	Lys	Leu	Leu	Asp	Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	210	215	220
Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val	Ser	Phe	Gly	Val	Val	Leu	Ala	Tyr	225	230	235
Lys	Ile	Lys	Leu	Val	Arg	Val	Pro	Glu	Val	Val	Thr	Val	Phe	Thr	Ile	245	250	255
Glu	Arg	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Thr	Ile	Ala	Glu	Arg	Trp	Val	260	265	270
Gln	Val	Ala	Asp	Lys	Leu	Asp	Arg	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	275	280	285
Ser	Val	Ile	Asn	Asp	Thr	Asn	Gly	Gly	Lys	Thr	Val	Arg	Ala	Ile	Phe	290	295	300
Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser	Arg	Asn	Leu	Val	Thr	Leu	Leu	Asn	305	310	315
Lys	Asp	Phe	Pro	Glu	Leu	Gly	Leu	Gln	Glu	Ser	Asp	Cys	Thr	Glu	Met	325	330	335
Ser	Trp	Val	Glu	Ser	Val	Leu	Tyr	Tyr	Thr	Gly	Phe	Pro	Ser	Gly	Thr	340	345	350
Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg	Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	355	360	365
Lys	Ile	Lys	Ser	Asp	Tyr	Val	Gln	Asn	Pro	Ile	Ser	Lys	Arg	Gln	Phe	370	375	380

Glu	Phe	Ile	Phe	Glu	Arg	Met	Lys	Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	
385					390					395					400	
Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met	Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	
				405					410					415		
Pro	Phe	Pro	His	Arg	Ser	Gly	Asn	Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	
			420				425						430			
Asn	Trp	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Glu	Asn	Arg	Tyr	Leu	Asn	Phe	
		435					440					445				
Thr	Arg	Leu	Met	Tyr	Asp	Tyr	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	
	450					455					460					
Arg	Glu	Ala	Phe	Leu	Asn	Tyr	Arg	Asp	Leu	Asp	Ile	Gly	Ile	Asn	Ser	
465					470					475					480	
His	Gly	Arg	Asn	Ala	Tyr	Thr	Glu	Gly	Met	Val	Tyr	Gly	His	Lys	Tyr	
			485					490						495		
Phe	Lys	Glu	Thr	Asn	Tyr	Lys	Arg	Leu	Val	Ser	Val	Lys	Thr	Lys	Val	
			500					505					510			
Asp	Pro	Asp	Asn	Phe	Phe	Arg	Asn	Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser	
		515					520					525				

Ser

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAGAAACTCG GAGACTTTCA CACAATGCCT AACCTCAAAC TCCGACCCCA AACATCCCAT 60
 CTCCCCCGCT ATCTTCTTCT CCGGAAATGG CTCCTACTCC TCCGTATTAC AAGCCAACAT 120
 CCGTAACCTC CGCTTCAACA CCACCTCAAC TCCGAAACCC TTCCTCATAA TCGCCGCAAC 180
 ACATGAATCC CATGTGCAAG CCGCGATTAC TTGCGGGAAA CGCCACAACC TTCAGATGAA 240
 AATCAGAAAGT GGAGGCCACG ACTACGATGG CTTGTCATAC GTTACATACT CTGGCAAACC 300
 GTTCTTCGTC CTCGACATGT TTAACCTCCG TTCGGTGGAT GTCGACGTGG 350

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGCATGGATC TCCGCCGAG CGACTCTCGG AGAGGTTTAT TATCGGATTT GGGAGAAAAG 60
 CAGAGTCCAT GGATTCCCCG CCGGAGTTTG ACCGACGGTT GGTGTTGGTG GGCATTTAAG 120
 CGGCGGTGGT TACGGTAACA TGGTGAGGAA GTTTGGATTA TCTGTGGATT ACGTTGAGGA 180
 TGCCAAGATC GTCGATGTAA ACNGTCGGGT TTAGATCGG AAAGCAATGG GTGAGGATCT 240
 GTTCTGGGCG ATTACCGGTG GAGGAGGAGG TAGCGTAC 278

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
TGGACATATT AGCGGAGGAG GATTCGGTAC AATAATGAGG AAATACGGTT TAGCGTCTGA   60
TAACGTTGTG GACGCACGTT TGATGGATGT AAATGGGAAA ACTCTTGACC GGAAAACGAT  120
GGGAGAGGAT TTGTTTTGGG CGCTTAGAGG CGGTGGAGCT GCGAGTTTTG GCGTTGTCTT  180
GTCGTGGAAG GTTAAGCTTG CTAGGGTTCC TGAAAAGGTA ACTTGTTTCA TAAGTCAACA  240
TCCGATGGGA CCTAGCATGA ACAAGCTTGT TCATAGATGG CAATCCATAG GATCAAGANN  300
GCTAGACGAA GATTTATTCA TCAGAGTCAA TATTGACAAC AGTCT                               345
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(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..695
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

GTTCGTTAAA ACCTATCCTN NANGGGCNAA AGNATATCAA AGNTTGNTTA NGNAACCCAA 60
NATTTCTGAA CTGGCCNCCT TCGGTGGTAT ATGNCNAAAN CCCTTGAATC TGCGNANCCN 120
ATTCCGCATA GAAACGGAAC CCTCTTCAAG ATTCTCTATT TACNCGAACT GNCTAGANNG 180
AATGACAAGA CATCGAGTAG NAAAATCAAC TGGATCAAAG AGATATACAA TTACATGGCG 240
CCTTATGTCT CAAGCAATCC AAGACAAGCA TATGTGAACT ACAGAGATCT AGACTTCGGA 300
CAGAACAAAGA ACAACGCAAA GGTTAACTTC ATTGAAGCTA AAATCTGGGG ACCTAAGTAC 360
TTCAAAGGCA ATTTTGACAG ATTGGTGAAG ATTAAAACCA AGGTTGATCC AGAGAACTTC 420
TTCAGGCACG AGCAGAGTAT CCCACCTATG CCCTACTAGA AGCTAGGTTC ATGAAACCAA 480
TAACATTATC AAAAATAAGR ATAAATGRTA ATTGTATACA ACATGATTCG KCTTCTTTA 540
TTTCAGACAA TGTGGACACT ACTCTAAANT AAAAWGTCNA TTTACCTTAA AAAAAAATA 600
ATCCCNNTA ANANAAAANT GGGGGGGCCN TTTTGGGGN TCCCGGTTT NGGACGGGGN 660
GCTTTNGGGG GGCTTGNNNT TTTTTTNGGN GCCCC 695

```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

TCTGTTTTNA GGCAGAGCAG AGGAAGTTGT TGCTTTGCTT GGTAAGGAGT TTCCTGAATT 60
NAGTTTAAAG AAGGAGAACT GTTCGGAGAT GACTTGGTTT CAGTCAGCTT TATGGTGGGA 120
TAATCGTGTT AACCTACTC ANATTGATCC WAAAGTGTTT CTCGATCGGA ATCTTGATAG 180

```

AGCGAATTTTC GGAAAGAGGA AATCGGATTA CGTTGCGAGT AAGATTCCTA GAGATGGGAT 240
 TAAGYCTTTT TCCAAGARGA TGMCTGACCT GGGGAAAAYC GGGCTTGTTT TTAAWCCGTA 300
 TGGTGGGAAA ATGGCGGAGG TTACGGTTAA CGCGACGCCG TTTCCNCACC GAAGCAAGCT 360
 TTTTAAGATT CAGTACTCGG TGACTIONGCA AGAAAACTCT NTCGAGATAG AGAAAGGGTT 420
 TCTTGAATCA GGCTAACGTC CTTATAGGTT CATGACCGGG TTTTNNAGCA AGANCCCTGG 480
 AATNCTTACT TNAAT 495

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..204
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AAATTAAAAC AAATCAATGT TGATATTGAA TCCAATAGTG CTTGGTTTCA ACCTGGTGCT 60
 ACGCTTGGTG AGCTTTACTA CAGAATTNCA GAGAAGAGCA AAATCCATGG ATTTCCNGCG 120
 GGTTTNTNCA CAAGCNTAGG CATAGGTGGG TATATNANAG GCGGTGGATA CGGTACCTTG 180
 ATGAGGAAGT ATGGTCTTNC GGGA 204

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..491
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

GAGATTTCTC GAGCAAGATA CTCCACTGAT GATCTTTGAG CCATTGGGTG GGAAAATCAG  60
CAAGATTTCA GAAACAGAAT CTCCATATCC ACACAGAAGA GGTAATCTGT ATAATATACA 120
GTACATGGTG AAATGGAAAG TGAATGANGT CGAGGAGATG AACAAACATG TCAGGTGGAT 180
GAGATCGTTA CACGATTACA TGA TCTCCGTA TGTTTCTAAA TCGCCGAGAG GAGCTTATTT 240
GANTTACAGA GATCTTGATT TGGGCTCGAC CAAAGGGATT AACACGGGTT TCGGAGATGC 300
AAGGAAATGG NNGGGTGAGN CTTTTTTTCAA AGGTAATTTT CAAGGGGTTA GGTTTTGGTT 360
AAAGGGGAGG TTTNNCCCAN CAAATTTTTTT TTCAGGANCC GGCCANGNTT TTCCCCCCCC 420
TNTTTTTTNGG NCCCCAATCN AAANCCCCGT TTTAAAAGGG GGGCCATTTC NTTTTTTNCA 480
NNTTAAAAGG G 491

```

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```
ATTGTGTCGT GAGGTAACT TTGACTTTAG TCAACGGTAC GAAGCCTGGT GAGAATACGG 60
TTTtagcgac TTTCATTGGG ATGTATTTAG GCCGGTCGGA TAAGCTGTTG ACCGTNATGA 120
ACCGGGATTT CCCGGAGTTG AAGCTGAAGA AAACCGATTN TACCGAGATG AGATGGATCG 180
ATTCGGTTCT GTTTTGGGAC GATTATCCGG TTGGTACACC GACTTCTGTG CTACTAAATC 240
CGCTAGTCGC AAAAAAGTTG TTCATGAAAC GAAATCGGA CTACGTGAAG CGTCTNATTT 300
TCGAGAACCC GATCTCNGT TTGATACTCA AGAAATTTGT AGAGGTTNNG AAAGTTAAAA 360
TNAATTTGGA TCCGCATTNN GGNANNNATG GTGAAACCCC NNGTTNT 407
```

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*
(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
ACGGCGTCGT ATTGGCCTAC AAAATAAACC TTGTTGAAGT CCCAGAAAAC GTCACCGTTT 60
TCAGAATCTC CCGGACGTTA GAACAAAATG CGACGGATAT CATTACCGG TGGCAACAAG 120
TTGCACCGAA GCTTCCCGAC GAGCTTTTCA TAAGANCAGT CATTGACGTA NAAACGGCAC 180
TGTTTCATNN CTCAAAGAC CGTCAGACAA CATTCATAGC AATGTTTCTA GGAGACACGN 240
CAACTCTACT GTCGATATTA AACCGGAGAT TCCCAGAATT GGGTTTGGTC CGGTCTGACT 300
```


GTACCGNAAC AAGCNNTTGG ATCCAATCTG TGCTATTTTT GGGACAAATA TCCCAGGTTG 360

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TCTTCACTGT CACCAAAACG TTAGAACAAG ACGCAAGATT GAAGACTATT TCTAAGTGGC 60
AACAAATTTT ATCCAAGATT ATTGAAGAGA TACACATCCG AGTGGTACTC AGAGCAGCTG 120
GAAATGATGG AAACAAGACT GTGACAATGA CCTACCTAGG TCAGTTTCTT GGCGAGAAAG 180
GCACCTTGCT GAAGGTTATG GAGAAGGCTT TTCCAGAACT AGGGTTAACT CAAAAGGATT 240
GTACTGAAAT GAGCTGGATT GAAGCCGCCC TTTTCCATGG TGGRTTTCCA ACAGGKTCTC 300
CTATTGAAAT TTTGCTTMAG CTCAAGTCGC CTYTAGGAAA AGRTTWCTTC AAAGCAACGK 360
CGGATTTTCGT TAAAGAACCT WTTCTGTGA TAGGGCTCAA AGGAATATTC AAAAGATTGA 420
TTGAAGG 427

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

GTTGTACTAT CATNGAAGAT TAAGTTAGTC GATGTTCCGT CCACGGTCAC CGNGTTTAAA 60
GTCCAGAAAC ATNAGGAGAA AGAGGCCGTT AGGNTCATCA ACAAGTGGCA GTATGTTGCG 120
GATAAGGTCC CTGAAGATCT TTTCATCAGC GCAACGTTGG NGAGATCAAA CGGAAACTCT 180
GTGCAGGCTT TGTTTACTGG ACTCTATCTT GGNCCGGTGA ATAATNTCTT GGCCTTGATG 240
GAAGAAAAGT TTCCAGANTT AGGTCTTGAT ATCCAAGNCT GCACAGAGAT GAGTTGGGCT 300
GAATCTGCAC TCTGGTNTNC TGNTTTCNCT AAAGGAGAGN CTCCTTGGGT GTTCNCGCG 360
GATCGGNAGC GGNCAATTTN TGGNCTTTCA AGGGGAAAGN CGGCTTTTTN CAAGAACCCG 420
NTACCCGGGG TTCAATT 437

```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

GCGGACCCTA TAGATCANNA TGTGCTACTG ANAGAAGAGG AAGCCAAGAA CAAGCCGGAG 60

```

ACAGATAAAT ATCTGAAATG GGNCGATANC GTTTACGAAT TTATGACNCC ATATGTTTCG 120
 AAATCTCCAA GAGGAGCTTA TGTCAATTTC AAGGATATGG ATTTGGGTAT GTATCTTGGA 180
 AAGAAGAAGA CAAAGTACGA GGAAGGAAAG AGTTGGGGAG TGAAGTATTT CAAGAACAAT 240
 TTCGAGAGAT TGGTGAGAGT GAAGACTAGG GTTGATCCAA CAGATTCTT CTGCGATGAA 300
 CAGAGCATTC CTCTGGTGAA CAAAGTTACC TGAAGATATC ATTTGAAGTT TTTTATTAGT 360
 CCCTTTTCTC TGTGAAATCA TCTGTGCGTG TTGAATATTA TGCCTCAAGT GTGTAACCTA 420
 TGTGTGTGAT TGTGAATTGT G 441

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGGCTTAAC ACAACGTCGT TTTGGGCCAA TTACCCGGCG GGTACACCCA AGAGCATCCT 60
 TCTAGATAGG CCTCCGACGA ATTCAGTGTC ATTTAAGAGT AAATCGGATT TTGTCAAAAA 120
 ACCAATACCC AAAAAAGGTT TAGAGAAGCT TTGGAAGACA ATGTTTAAAT TCAACAGTAG 180
 CGTCTCGTTG CAATTCAACC CTTACGGTGG AGTGATGGAC CGGATTCCGG CAACGGCCAC 240
 CGCTTTTCCT CATCGGAAAG GAAACTTGTT CAAGGTTCAA TACNCTACGA TGTGGTTTGA 300
 CGCAAACGCC ACACAGAGTA GCCNGGCTAT GATGAATGAG CTTTTTGAGG TGGCGGGACC 360
 GTACGTGNGT CAAGTAAACC CGAGANANGG CTTCTTTTAA NTTTCAGAGNC CATCGNTNTT 420
 NGGAGCAANN CCAAGTGGGG GGGNCCAACC GGGGGNTNAA ANCNNAGNTC TTNGGGGGGCC 480

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
NGGGAATTGC NCGAGGNAAG TTGTACCCAA TTCCTGGACC ACCATTGGTT TCCCAAGAAN   60
CCCGAGACAA CCGTTTTTCA ATNACCGTGA TGTTGATTG GGTATTAATT CTCATAATGG 120
TAAAATCAGT AGTTATGTGG AAGGTAAACG TTACGGGAAG AAGTATTTTCG CAGGTAATTT 180
CGAGAGATTG GTGAAGATTA AGACGAGAGT TGATAGTGGT AATTTCTTTA GGAACGAACA 240
GAGTATTCCT GTGTTACCAT AAGTGTATTT ATTTGATTAT TGGTTAGTGA AATTTGTTGT 300
TGTATAATGA TTATATGTCG TATTTTTATT TATTATTAGT AATTTATAAA GTTTGATATT 360
AAATACAAAT AGTATAATAA GATAGTTTCT TTTAGTAAAA                        400
```

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
CAACTCTAAT GGGAAACACCT ACTTCGATCG AATGTCGATG GGGGAAGAGC TTTTCTGGGC   60
GGTTCGAGGA GGTGGAGCCG CGAGTTTCGG CATCGTGATG GGATACAAAA TCCGGTTGGT  120
TCCGGTTCCG GAGAAAGTTA CGGTTTTTTAG CGTCGGAAAA ACCGTCGGAG AAGGAGCCGT  180
TGATCTTATA ATGAAGTGGC AGAACTTCTC TCATAGTACG GNTCGGAATT TTTTTGTGAA  240
GCTGANTTTT GANTTTAGTC AACGGTGCAA AGCCGGGTGA AAAAAAGGTT TTAGNGNCTT  300
TCANTTTGGN TGNAANCTTG GGGGTTTTAT NAGAACGGTT AACCGGGATT NANCCCGNGT  360
TTTCCCGGGG TTAAACCTT NGG                                           383
```

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
ATCAATGTTT TACTAAACG TACACGAGCA TCGTTGGCTT TCAAGGCTAA ATCTGATTTT   60
NTTCAAGAAC CGATNCCTAA AACC GCGATT TCGAAGCTTT GGAGACGGTT GCAAGAACCG  120
```

GAAGCAGAGC ATGCTCAGCT AATTTNCACN CCATTTGGTG GTAAAATGAG TNAGATTGCA 180
 GATTACGAAA CACCATTTCC GCATAGGAAG GGGAATATAT ATNAGATTCA GTACTTGAAT 240
 TACTGGAGAG GAGACGTGAA AGAGAAGTAT ATTGAGATNG GTGGAGGAGA GTTTACGGTT 300
 GNTATNAGTA AGTTTTTTTG CGAAGTNTNC CNAGAGGNGN CTTNNTNTAA ACCT 354

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..403
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TTTTTTAGTA CACTAATAAT CAAATGGAAT GAGAAATGAA GCCACAAAAG TATCTGCAAT 60
 CAAAATATCC TGCTATCTCC ATCTCAAGCT CTCAATAGTA TCCTCTCCGA AAGTGAAATC 120
 AACATTTCAA ACTCTATTTT TGGTGGAAT CGATAGACTG ATTCCTCTGA TGAACCAGAA 180
 GTTTCGGAA CTCGGCTTAC GATCTCAAGA CTGTTCGGAA ATGAGCTGGA TCGAATCGAT 240
 AATGTTCTTC AACTGGAGAT CAGGACAGCC GTTAGAGATT TTGCTCAACA GAGACCTAAG 300
 GATTTCGAGGA TCAGTATTTT AAAGCAAAGT CAGGATTATG GTTCAAAAAC CCGTTCCTGA 360
 AAACGTTTTT CGAAGAGGTA TCCAAGGGGT TTCTCGAGCA AGT 403

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
GAGATGAGTT GGATTAANTC TGTACTCTGG TTTGCTGATT TCCCTAAAGG AGAATCTCTT 60
NGTGTCTCTCA CGAATCGTAA GCGTACATCT CTATCTTTNA AAGGCAAAGA TGATTTTATC 120
CAAGAACCGA TACCCGAGGC TGCAATTNAA GAGATATGGA GGCGATTAGA AGCCCCNAG 180
GCTCGGCTTG GAAAGATCAT ATTA ACTCCA TTTGGTGGGA AAATNAGTGA AATGGCAGAG 240
TACGTANCAC CATTCCCACA                                     260
```

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: ecotype Columbia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
CTCTTGCATA TTCGCTGCAA GGATGGGAAA TTCAAAACCA CTCCTACAA TTTTGTAT 60
```

TATAGTTTCA GTCTTGTATT TTTAATTCTA TTGCATAACA CCAACTTCTT CATCAGCCTC 120
CATCCAAGAT CAATTCATAA ACTGTGTCAA AAGAAACACA CATGTTTCTT TTCCACTCGA 180
GAAAACGTTA TTCACCCCTG CGAAAAACGT CTCTTTGTTC AACCAAGTCC TTGANTCGAC 240
GGCTCAAAAT CTCCAGTTCT TGGCAAAATC CATGCCTAAA CCGGGRTTCA TATTCAGACC 300
GATTCAACCAG TCTCAAGTCC AAGSTTCCAT CATTTGTTCA AMGRAACTCG GGNTTCATTT 360
TNGTGTTTGA NGTGGCGGTC ACGATTTTCG AGGCCTTTGT NTTTATGTTT CACGGTTTGA 420
AAAAACCGTT TATATTACTC GGCCTGTCAA ANTTGNANNC AAAATCANAT GTTGGATATT 480
GNATTCCAAA TAGGTNCTTG GGGTNAACCT GGTGGCTANC GTTTGGTGAG CTTTTACTTT 540
CAAGAATTTG CANGNGGANG TGCAAAGATT CCATGGGATT TCCCGGGGGG TTTNTTGCAC 600
AATGT 605

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AACACAAAAC TCTTCCATTT GGCTTCTCTC TTGCATATTC GTTGCAAGGA TGGGAAATTC 60
AAAACCACTC CCTACAATTN CTTGTATTAT CGTTTCAGTC TTGTATTTN NATTCTATTG 120
CATAACACCA ACTTCTTCAT CAGCCTCCAT CCAAGNTCAA TTCATAAACT GTGTCAAAAG 180
GAACACACAT GTTTCTTTTC CACTCGAGNA AACGGTATTC ACTCCTGCGG AAAACGGCTC 240
TNTTATTCAA CGGGTCCNTG AATCGACGGG TCAAAATCTC CAGTTCTTGG NAAAATCCAT 300

GNCTAAACCG GGGTTCATAT TCAGGCCGGT TCACCAGTCT CAAGTCCAAG NTTCCATCAT 360
 TTGTTCAAAG GAACTCGGGA TTCATTTCCG CGNTAGAAGT GGCGGGCANN GGTTCGGGG 420
 CCTGTCTNTT GNTTANGGN AGGAAAACCG GTTNTATTNC TCGG 464

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..386
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCGGGAGCCC ANGNTAAATT ANNTGAAAAT GGGGNCGNAT ANCCGTTTAC NGAATTTTAT 60
 GACNCCCAAT ATGTTTCGAA ATCTCAAAGA NNGGGANCTT ATGTCAATTT CAAGGATATG 120
 GATTTGGGTA TGTATCTTGG AAAGNAGAAG ACAAAGTACG AGGAAGGAAA GAGTTGGGGA 180
 GTGAAGTATT TCAAGAACAA TTTCGAGAGA TTGGTGAGAG TGAAGACTAG GGTGATCCN 240
 ACAGATTTCN TCTGCGATGA ACAGAGCATT CCTCTGGTGN ACAAAGTTAC CTGAAGATAT 300
 CATTTGAAGT TTTTATTAG TCCCTTTTCT CTGTGAAATC ATCTGTGCGT GTTGAATANT 360
 ATGCGTCAAG TGTGTAACCT ATGTGT 386

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
TACCATAGGG AGGTGGTGNA AGATTTTGTG TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60
TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120
TTCATTGAAG CTAAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180
AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCCACCT 240
ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300
ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCAGA CAATGTGGAC ACTACTCTAA 360
ATAAAAATGTC ATTTACC 377
```

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

TACCATAGGG AGGTGGTGNA AGATTTTGTGTA TGTAGNCTTA GGGGAAGGCG AGTAGTATGG 60
 TGGTGGTGGG GAGCTGTAAA CGTATGGTGG TGGTGGAGAT TTGTATGTGG GCTGGTTAAC 120
 TTCATTGAAG CTAAAATCTG GGGACCTAAG TACTTCAAAG GCAATTTTGA CAGATTGGTG 180
 AAGATTAAAA CCAAGGTTGA TCCAGAGAAC TTCTTCAGGC ACGAGCAGAG TATCCCACCT 240
 ATGCCCTACT AGAAGCTAGG TTCATGAAAC CAATAACATT ATCAAAAATA AGAATAAATG 300
 ATAATTGTAT ACAACATGAT TCGTCTTTCT TTATTTTCAGA CAATGTGGAC ACTACTCTAA 360
 ATAAAATGTC ATTTACC 377

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..346
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAGCTGTGGA TATGGTCACA AATGGCAATC GGTGGTCCG AAAACTGATC CGAATCTTTT 60
 TATGAGAATN TTGATTCAAC CAGTGACGAG GAAGAAGGTA AAGACTGTGA GAGCTTCTNT 120
 GGTGGCCCTN TTTTNAGGCN AGACAGATGA AGTTTTTGCT TTCCTTAGTA AGGAGTTTCC 180
 TGAATTGGGT TTAAAGAAGG AGAATTNTTC GGAGATGACT TGGTTTCANT CTGCTTTATG 240
 GTGGGACAAT CGTCTTAATG CTA CTCAGGT TGATCCTAAA GTNTTCTTG ATCGGAATCT 300
 CGATACCTCG AGTTTCGGTA AGAGGAAATC GGATTACGTC GCGACT 346

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..261
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ATGGGGTGAG ACTTATTTCA AAGGTAATTT CAAGAGATTA GGTTCGGTTA AAGGGAAGNT 60
TGATCCAACA AATTTCTTCA GGAACGAACA GAGTATTCCT CCTCTGTTTT GAGTCCTCAA 120
TACAAAACCA GATATAAAAG ATGTCATTTT ATTTTTTCAA TTATAATAGA TAATGTAAGT 180
TTCTGCTACA ATTGTAAAAG TGAGATGTAC CCAATACGGT TTAAGCGGAC CGAGAATAGT 240
CAATTCAAAG ACCAAATTCT G 261
```

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
 - (B) STRAIN: ecotype Columbia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```
GCTCAAAGGA CTAACCATGA AACTTCCTC AAGTGTCTCT CTCACCGANT CAACGAGGAC 60
GACTCAAGAN TTATACACAC ATCAAAGAT CCTTCGTATT TNTCAATCTT GATTTCTTCC 120
ATACAAAATC CAAGTTTCTC TGTTCCTGAA ACACCTAAAC CGGTTTCAAT CATCACTCCG 180
GTTCAAGCCA CCGATGTTCA ATCTACGNTT AAATNCGCAC GGNCTTCACG GGTATACACA 240
ATCAGGGCTA GGAGTGGTNG TCATGACTAC GGAGGTTTAT CTTTACATTG GCTTAAAAAN 300
CANNCCGTTT GTTNNTCATT GATTTNNAGA AATCTTCCGG GCTTATTTAA CATNTAAGAT 360
GTTTGATAAN CCGGNCCNG TTTGGGGTTC AAATCCCGGT GGCTTACAAA NTTNGGGGGA 420
ATTGTNCCTA TGAGGTTTGG AAAATTAANG CAAATNTTTT TGGGCCTTCC CGGCCGGT 478
```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```
GGCCGTTAGG ATCATCAAGA AATGGCAATA TGCTGCAGAT AAGGTTCTTG ATGATCTTTT 60
CATTAGGACA ACATTGGAGA GATCAAACAA GAACGCAGTA CACGCTTTGT TCACTGGACT 120
ATATATTGGT CCGGTGAACA ATCTATTGGC GTTGATGGAA GAAAAGTTTC CGGAACTAGG 180
TCTTGAGAAA GAAGGTTGTG AAGAGATGAG TTGGATTGAG TCTGTACTCT GGTTCGCTGA 240
TTTCCCTAAA GGAGAATCTC TTGGTGTCT CACGAATCGT GAGCGTACAT CTCTATCTTT 300
CAAAGGCAAA GATGATTTTG TCCAAGAACC GATACCCGAG GCTGCAATTC AAGAGATATG 360
```

GAGGCGATTA GAAGCCCCCG AGGCTCGGCT TGGAAAGATC ATATTA ACTC CATT TGGGTG 420
 NGGNAAAATG AGTGAAATGG CAGAGNCCGA ACCACCAATT CCCACANNCG AGGGAGGGGA 480
 ACCCCTNTGN GGNTCAGAAT GTGGTTCCTG GNNNNNAAGN GGGNGCCAGN ACCAANCCGG 540
 GNCNGTAAAN CNTGNAATGG GCCNAACCCG TNCCGGATT 579

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Oryza sativa*
- (B) STRAIN: Nipponbare, subsp. japonica
- (D) DEVELOPMENTAL STAGE: etiolated shoot (8 days old)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGTCCTGGAA GGTCCGCCTC GTGCAGGTTN CGACGACGGT GACGGTGTTT CTCGTCGGGA 60
 GGAACGTCGA CCAGGGCGCC GCNGACGTCG TCGCCAGATG GCAAGACGTC GCGCCGAGCC 120
 TCCCTCCCGA GCTCACCATA CGGGTGATCG TNCGAGGGCA GCGCGCCACG TTCCAGTCGC 180
 TGTACCTCGG CTCGTGCGCC GACCTGGTGC CGACGATGAG CAGCATGTTC CCGGAGCTCG 240
 GGATGACGAT TG 252

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /label= Ambiguous
/note= "Xaa = Cys or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20..21
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa-Xaa probably is Ser-Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```
Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Xaa Leu Asn Asn Arg
1              5              10              15
Ala Asp Pro Xaa Xaa
                20
```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa = probably Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa = probably Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa = probably Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /label= ambiguous
/note= "Xaa = probably Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Xaa Ile Xaa Val Xaa Ile Glu Asp Glu Thr Ala Xaa Val Gln Ala Gly
1 5 10 15
Ala Thr Leu Gly Glu Val Tyr Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactuca sativa
- (B) STRAIN: lollo bionda

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Tyr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ACTTCTACTT CTATTATTGA TAGGTTTACT CA

32

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactuca sativa
(B) STRAIN: lollo bionda

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACT TCT ACT TCT ATT ATT GAT AGG TTT ACT CAA TGT CTA AAC AAC CGA	48
Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg	
1 5 10 15	
GCT GAC CCT TCT TTC CCG CTC AGT GGA CAA CTT TAC ACT CCC GAT AAC	96
Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn	
20 25 30	
TCC TCT TTT CCA TCC GTC TTG CAA GCT TAC ATC CGG AAC CTC CGA TTC	144
Ser Ser Phe Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe	
35 40 45	
AAT GAA TCC ACG ACT CCC AAA CCC ATC TTA ATC ATC ACC GCC TTA CAC	192
Asn Glu Ser Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His	
50 55 60	
CCT TCA CAC ATT CAA GCA GCT GTT GTG TGC GCC AAA ACA CAC CGC CTG	240
Pro Ser His Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu	

65	70	75	80	
CTA ATG AAA ACC AGA AGC GGA GGC CAT GAT TAT GAG GGG CTT TCC TAT				288
Leu Met Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr				
	85	90	95	
GTG ACC AAT TCG AAC CAA CCC TTT TTT GTT GTT GAC ATG TTC AAC TTA				336
Val Thr Asn Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu				
	100	105	110	
CGC TCC ATA AAC GTG AGT ATT GAA GAT GAA ACT GCA TGG GTC CAA GCC				384
Arg Ser Ile Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala				
	115	120	125	
GGC GCC ACC CTC GGA GAA GTT				405
Gly Ala Thr Leu Gly Glu Val				
	130	135		

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Thr Ser Thr Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg				
1	5	10	15	
Ala Asp Pro Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn				
	20	25	30	
Ser Ser Phe Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe				
	35	40	45	
Asn Glu Ser Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His				
	50	55	60	
Pro Ser His Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu				
	65	70	75	80
Leu Met Lys Thr Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr				
	85	90	95	
Val Thr Asn Ser Asn Gln Pro Phe Phe Val Val Asp Met Phe Asn Leu				
	100	105	110	
Arg Ser Ile Asn Val Ser Ile Glu Asp Glu Thr Ala Trp Val Gln Ala				
	115	120	125	

Gly Ala Thr Leu Gly Glu Val
130 135

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CACGTTTATG GAGCGTAAGT TGAAC

25

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CACCCTTCAC ACATTCAAGC AGC

23

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1981 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactuca sativa*

(B) STRAIN: lollo bionda

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..1626

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(372, "g")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(379, "g")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(786, "t")

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: replace(1105..1106, "ga")

(D) OTHER INFORMATION: /note= "also possible "gg" and "aa"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACAAAA ATG GCA ATT ACC TAT TCT TTC AAC TTC AAA TCT TAT ATT TTT	48
Met Ala Ile Thr Tyr Ser Phe Asn Phe Lys Ser Tyr Ile Phe	
1 5 10	
CCT CTC CTC CTT GTC TTG CTC TCT ACC CAT TCA TCA GCG ACT TCA ACT	96
Pro Leu Leu Leu Val Leu Leu Ser Thr His Ser Ser Ala Thr Ser Thr	
15 20 25 30	
TCC ATT ATA GAT CGC TTC ACC CAA TGT CTA AAC AAC CGA GCT GAC CCT	144
Ser Ile Ile Asp Arg Phe Thr Gln Cys Leu Asn Asn Arg Ala Asp Pro	
35 40 45	
TCT TTC CCG CTC AGT GGA CAA CTT TAC ACT CCC GAT AAC TCC TCT TTT	192
Ser Phe Pro Leu Ser Gly Gln Leu Tyr Thr Pro Asp Asn Ser Ser Phe	
50 55 60	
CCA TCC GTC TTG CAA GCT TAC ATC CGG AAC CTC CGA TTC AAT GAA TCC	240
Pro Ser Val Leu Gln Ala Tyr Ile Arg Asn Leu Arg Phe Asn Glu Ser	
65 70 75	
ACG ACT CCC AAA CCC ATC TTA ATC ATC ACC GCC TTA CAC CCT TCA CAC	288
Thr Thr Pro Lys Pro Ile Leu Ile Ile Thr Ala Leu His Pro Ser His	
80 85 90	
ATT CAA GCA GCT GTT GTG TGC GCC AAA ACA CAC CGC CTG CTA ATG AAA	336
Ile Gln Ala Ala Val Val Cys Ala Lys Thr His Arg Leu Leu Met Lys	
95 100 105 110	
ACC AGA AGC GGA GGC CAT GAT TAT GAG GGG CTT TCC TAT GTG ACC AAT	384

Thr	Arg	Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Val	Thr	Asn	
				115					120					125		
TCG	AAC	CAA	CCC	TTT	TTT	GTT	GTT	GAC	ATG	TTC	AAC	TTA	CGC	TCC	ATA	432
Ser	Asn	Gln	Pro	Phe	Phe	Val	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	
			130					135					140			
AAC	GTG	AGT	ATT	GAA	GAT	GAA	ACT	GCA	TGG	GTC	CAA	GCT	GGT	GCG	ACT	480
Asn	Val	Ser	Ile	Glu	Asp	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	
			145				150					155				
CTT	GGT	GAA	GTC	TAC	TAC	CGA	ATA	GCA	GAG	AAA	AGC	AAC	AGT	CAT	GCT	528
Leu	Gly	Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Ser	His	Ala	
			160			165					170					
TTT	CCG	GCT	GGC	GTT	TGC	CCT	ACT	GTT	GGA	GTT	GGT	GGC	CAT	TTT	AGT	576
Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	
175					180				185						190	
GGT	GGT	GGT	TAT	GGT	AAC	TTG	ATG	GGA	AAA	TAC	GGC	CTT	TCT	GTT	GAC	624
Gly	Gly	Gly	Tyr	Gly	Asn	Leu	Met	Gly	Lys	Tyr	Gly	Leu	Ser	Val	Asp	
				195				200						205		
AAT	ATT	GTC	GAT	GCT	CAG	TTA	ATC	GAT	GTG	AAT	GGT	AAA	CTT	CTG	AAT	672
Asn	Ile	Val	Asp	Ala	Gln	Leu	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asn	
			210					215					220			
CGG	AAA	TCA	ATG	GGT	GAA	GAT	CTT	TTT	TGG	GCC	ATC	ACA	GGT	GGT	GGT	720
Arg	Lys	Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Thr	Gly	Gly	Gly	
			225				230					235				
GGT	GTC	AGC	TTT	GGT	GTG	GTT	GTA	GCG	TAC	AAG	ATC	AAA	CTG	GTT	CGT	768
Gly	Val	Ser	Phe	Gly	Val	Val	Val	Ala	Tyr	Lys	Ile	Lys	Leu	Val	Arg	
	240					245					250					
GTT	CCT	ACC	ACT	GTG	ACC	GTT	TTT	AAC	GTA	CAA	AGA	ACA	TCC	GAG	CAG	816
Val	Pro	Thr	Thr	Val	Thr	Val	Phe	Asn	Val	Gln	Arg	Thr	Ser	Glu	Gln	
255					260					265					270	
AAC	CTA	AGC	ACC	ATA	GCC	CAC	CGA	TGG	ATA	CAA	GTT	GCG	GAT	AAG	CTC	864
Asn	Leu	Ser	Thr	Ile	Ala	His	Arg	Trp	Ile	Gln	Val	Ala	Asp	Lys	Leu	
				275				280						285		
GAT	AAT	GAC	CTT	TTC	CTT	CGA	ATG	ACC	TTT	AAC	GTG	ATA	AAC	AAC	ACA	912
Asp	Asn	Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	Asn	Val	Ile	Asn	Asn	Thr	
			290				295						300			
AAT	GGC	GAA	AAG	ACG	ATA	CGT	GGT	TTG	TTT	CCA	ACA	CTG	TAC	CTC	GGA	960
Asn	Gly	Glu	Lys	Thr	Ile	Arg	Gly	Leu	Phe	Pro	Thr	Leu	Tyr	Leu	Gly	
			305				310					315				
AAC	TCT	ACC	GCT	CTT	GTT	GCC	CTC	CTG	AAC	AAG	GAT	TTC	CCT	GAA	TTA	1008
Asn	Ser	Thr	Ala	Leu	Val	Ala	Leu	Leu	Asn	Lys	Asp	Phe	Pro	Glu	Leu	
			320			325					330					

GGT GTA GAA ATT TCA GAT TGT ATT GAA ATG AGT TGG ATC GAG TCT GTT	1056
Gly Val Glu Ile Ser Asp Cys Ile Glu Met Ser Trp Ile Glu Ser Val	
335 340 345 350	
CTT TTC TAC ACA AAC TTC CCC ATT GGT ACT CCG ACC ACT GCT CTT CTA	1104
Leu Phe Tyr Thr Asn Phe Pro Ile Gly Thr Pro Thr Thr Ala Leu Leu	
355 360 365	
AGC CGT ACA CCT CAA AGA CTA AAC CCA TTC AAA ATC AAA TCT GAT TAC	1152
Ser Arg Thr Pro Gln Arg Leu Asn Pro Phe Lys Ile Lys Ser Asp Tyr	
370 375 380	
GTA AAA AAC ACT ATT TCC AAA CAG GGA TTC GAA TCC ATA TTT GAA AGG	1200
Val Lys Asn Thr Ile Ser Lys Gln Gly Phe Glu Ser Ile Phe Glu Arg	
385 390 395	
ATG AAA GAA CTC GAA AAC CAA ATG CTA GCT TTC AAC CCT TAT GGT GGA	1248
Met Lys Glu Leu Glu Asn Gln Met Leu Ala Phe Asn Pro Tyr Gly Gly	
400 405 410	
AGA ATG AGC GAA ATT TCC GAA TTT GCA AAG CCT TTT CCC CAT CGA TCA	1296
Arg Met Ser Glu Ile Ser Glu Phe Ala Lys Pro Phe Pro His Arg Ser	
415 420 425 430	
GGG AAT ATA GCG AAG ATC CAA TAC GAA GTA AAC TGG GAT GAA CTT GGC	1344
Gly Asn Ile Ala Lys Ile Gln Tyr Glu Val Asn Trp Asp Glu Leu Gly	
435 440 445	
GTT GAA GCA GCC AAT CGG TAC TTG AAC TTC ACA AGG GTG ATG TAT GAT	1392
Val Glu Ala Ala Asn Arg Tyr Leu Asn Phe Thr Arg Val Met Tyr Asp	
450 455 460	
TAT ATG ACT CCG TTT GTT TCT AAG AAC CCC AGG GAA GCA TTT CTG AAC	1440
Tyr Met Thr Pro Phe Val Ser Lys Asn Pro Arg Glu Ala Phe Leu Asn	
465 470 475	
TAC AGG GAT TTA GAT ATT GGT GTC AAC AGT CAT GGC AAG AAT GCT TAC	1488
Tyr Arg Asp Leu Asp Ile Gly Val Asn Ser His Gly Lys Asn Ala Tyr	
480 485 490	
GGT GAA GGA ATG GTT TAT GGG CAC AAG TAT TTC AAA GAG ACG AAT TAT	1536
Gly Glu Gly Met Val Tyr Gly His Lys Tyr Phe Lys Glu Thr Asn Tyr	
495 500 505 510	
AAG AGG CTA ACG ATG GTG AAG ACG AGG GTT GAT CCT AGC AAT TTT TTT	1584
Lys Arg Leu Thr Met Val Lys Thr Arg Val Asp Pro Ser Asn Phe Phe	
515 520 525	
AGG AAT GAG CAA AGT ATC CCA ACT TTG TCA TCT TCA TGG AAG	1626
Arg Asn Glu Gln Ser Ile Pro Thr Leu Ser Ser Ser Trp Lys	
530 535 540	
TAAATTCTAA ATTCACTTGT GAAATTGAAT AAAAGTATGG CTTTTTCAAG GTCATGGTAT	1686

CCAGATTCAG	ATGATATTGA	TATAATTTTG	ACTTGTATTT	ATACAAACAA	AATTATATTA	1746
TATTTTTCTG	AATTTAGATT	TTCCATTCTT	TGGAAAAATA	TACGAACATT	GATGTTGATA	1806
TTTTTAAGAA	TTATAGATTT	TGAACATTGT	GAACAATGAA	TAAACCGAGG	ACTTCCCTTG	1866
GGTTTTTTTT	ATAAGTATGT	AATAGCATGT	CTTTAATCAA	GATAACCGAT	CATTGGATGC	1926
AATTTATTAT	TATAAACCTT	ATTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA	1981

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

Met	Ala	Ile	Thr	Tyr	Ser	Phe	Asn	Phe	Lys	Ser	Tyr	Ile	Phe	Pro	Leu
1				5					10					15	
Leu	Leu	Val	Leu	Leu	Ser	Thr	His	Ser	Ser	Ala	Thr	Ser	Thr	Ser	Ile
			20					25					30		
Ile	Asp	Arg	Phe	Thr	Gln	Cys	Leu	Asn	Asn	Arg	Ala	Asp	Pro	Ser	Phe
		35					40					45			
Pro	Leu	Ser	Gly	Gln	Leu	Tyr	Thr	Pro	Asp	Asn	Ser	Ser	Phe	Pro	Ser
	50					55					60				
Val	Leu	Gln	Ala	Tyr	Ile	Arg	Asn	Leu	Arg	Phe	Asn	Glu	Ser	Thr	Thr
65					70					75					80
Pro	Lys	Pro	Ile	Leu	Ile	Ile	Thr	Ala	Leu	His	Pro	Ser	His	Ile	Gln
			85						90					95	
Ala	Ala	Val	Val	Cys	Ala	Lys	Thr	His	Arg	Leu	Leu	Met	Lys	Thr	Arg
			100					105					110		
Ser	Gly	Gly	His	Asp	Tyr	Glu	Gly	Leu	Ser	Tyr	Val	Thr	Asn	Ser	Asn
		115					120					125			
Gln	Pro	Phe	Phe	Val	Val	Asp	Met	Phe	Asn	Leu	Arg	Ser	Ile	Asn	Val
	130					135					140				
Ser	Ile	Glu	Asp	Glu	Thr	Ala	Trp	Val	Gln	Ala	Gly	Ala	Thr	Leu	Gly
145					150					155					160
Glu	Val	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Ser	His	Ala	Phe	Pro
				165					170					175	

Ala	Gly	Val	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	His	Phe	Ser	Gly	Gly		
			180					185					190				
Gly	Tyr	Gly	Asn	Leu	Met	Gly	Lys	Tyr	Gly	Leu	Ser	Val	Asp	Asn	Ile		
		195					200					205					
Val	Asp	Ala	Gln	Leu	Ile	Asp	Val	Asn	Gly	Lys	Leu	Leu	Asn	Arg	Lys		
	210					215					220						
Ser	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Thr	Gly	Gly	Gly	Gly	Val		
225					230					235					240		
Ser	Phe	Gly	Val	Val	Val	Ala	Tyr	Lys	Ile	Lys	Leu	Val	Arg	Val	Pro		
			245						250					255			
Thr	Thr	Val	Thr	Val	Phe	Asn	Val	Gln	Arg	Thr	Ser	Glu	Gln	Asn	Leu		
		260						265					270				
Ser	Thr	Ile	Ala	His	Arg	Trp	Ile	Gln	Val	Ala	Asp	Lys	Leu	Asp	Asn		
		275					280					285					
Asp	Leu	Phe	Leu	Arg	Met	Thr	Phe	Asn	Val	Ile	Asn	Asn	Thr	Asn	Gly		
	290					295					300						
Glu	Lys	Thr	Ile	Arg	Gly	Leu	Phe	Pro	Thr	Leu	Tyr	Leu	Gly	Asn	Ser		
305					310					315					320		
Thr	Ala	Leu	Val	Ala	Leu	Leu	Asn	Lys	Asp	Phe	Pro	Glu	Leu	Gly	Val		
			325						330					335			
Glu	Ile	Ser	Asp	Cys	Ile	Glu	Met	Ser	Trp	Ile	Glu	Ser	Val	Leu	Phe		
			340					345					350				
Tyr	Thr	Asn	Phe	Pro	Ile	Gly	Thr	Pro	Thr	Thr	Ala	Leu	Leu	Ser	Arg		
		355					360					365					
Thr	Pro	Gln	Arg	Leu	Asn	Pro	Phe	Lys	Ile	Lys	Ser	Asp	Tyr	Val	Lys		
	370					375					380						
Asn	Thr	Ile	Ser	Lys	Gln	Gly	Phe	Glu	Ser	Ile	Phe	Glu	Arg	Met	Lys		
385					390					395					400		
Glu	Leu	Glu	Asn	Gln	Met	Leu	Ala	Phe	Asn	Pro	Tyr	Gly	Gly	Arg	Met		
			405						410					415			
Ser	Glu	Ile	Ser	Glu	Phe	Ala	Lys	Pro	Phe	Pro	His	Arg	Ser	Gly	Asn		
			420					425					430				
Ile	Ala	Lys	Ile	Gln	Tyr	Glu	Val	Asn	Trp	Asp	Glu	Leu	Gly	Val	Glu		
		435					440					445					
Ala	Ala	Asn	Arg	Tyr	Leu	Asn	Phe	Thr	Arg	Val	Met	Tyr	Asp	Tyr	Met		
	450					455					460						

Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Glu	Ala	Phe	Leu	Asn	Tyr	Arg
465					470					475					480
Asp	Leu	Asp	Ile	Gly	Val	Asn	Ser	His	Gly	Lys	Asn	Ala	Tyr	Gly	Glu
			485						490					495	
Gly	Met	Val	Tyr	Gly	His	Lys	Tyr	Phe	Lys	Glu	Thr	Asn	Tyr	Lys	Arg
		500						505						510	
Leu	Thr	Met	Val	Lys	Thr	Arg	Val	Asp	Pro	Ser	Asn	Phe	Phe	Arg	Asn
		515					520						525		
Glu	Gln	Ser	Ile	Pro	Thr	Leu	Ser	Ser	Ser	Trp	Lys				
	530					535					540				

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTAATGATC TCCTTTCTTG TTTGACC

27

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGAGCGGCCG CTATATTACA ACTTCTCCAC CATCACTCCT C

41

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GGTGATGTTA ATGATAATCT CCTC

24

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

AGAGCGGCCG CTACAATTCC TTCAACATGT AAATTCCTC

40

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACTTCCCGTA GAAACTCGGA GACTTTCACA CAATGC

36

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TCCATCCAAG ATCAATTCAT AAAGTGTGTC

30

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGAGCGGCCG CTTTCATGAA CCTAGCTTCT AGTAGG

36

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAGCGGCCG CGAAATGGCC CCCCTTTTAA AACGGGG

37

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGAGCGGCCG CAAATGATAT CTTCAGGTAA CTTTGTTTAC

40

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGAGCGGCCG CATAATCAAA TAAATACACT TATGGTAACA CAG

43

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGAGCGGCCG CTGGTTTTGT ATTGAGGACT CAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1757 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: Colombia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1..570, 801..1754)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

ACT	TCC	CGT	AGA	AAC	TCG	GAG	ACT	TTC	ACA	CAA	TGC	CTA	ACC	TCA	AAC	48
Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn	
1				5				10						15		
TCC	GAC	CCC	AAA	CAT	CCC	ATC	TCC	CCC	GCT	ATC	TTC	TTC	TCC	GGA	AAT	96
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn	
			20					25						30		
GGC	TCC	TAC	TCC	TCC	GTA	TTA	CAA	GCC	AAC	ATC	CGT	AAC	CTC	CGC	TTC	144
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe	
			35					40						45		
AAC	ACC	ACC	TCA	ACT	CCG	AAA	CCC	TTC	CTC	ATA	ATC	GCC	GCA	ACA	CAT	192
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His	
			50					55						60		
GAA	TCC	CAT	GTG	CAA	GCC	GCG	ATT	ACT	TGC	GGG	AAA	CGC	CAC	AAC	CTT	240
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
						70					75				80	
CAG	ATG	AAA	ATC	AGA	AGT	GGA	GGC	CAC	GAC	TAC	GAT	GGC	TTG	TCA	TAC	288
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	
						85					90				95	
GTT	ACA	TAC	TCT	GGC	AAA	CCG	TTC	TTC	GTC	CTC	GAC	ATG	TTT	AAC	CTC	336
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	
						100								110		
CGT	TCG	GTG	GAT	GTC	GAT	GTG	GCA	AGT	AAG	ACC	GCG	TGG	GTC	CAA	ACC	384
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	
						115								125		
GGT	GCC	ATA	CTC	GGA	GAA	GTT	TAT	TAC	TAT	ATA	TGG	GAG	AAG	AGC	AAA	432
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	
						130								140		
ACC	CTA	GCT	TAT	CCC	GCC	GGA	ATT	TGT	CCC	ACG	GTT	GGT	GTC	GGT	GGC	480
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	
						145								150		
CAT	ATC	AGT	GGT	GGA	GGT	TAC	GGT	AAC	ATG	ATG	AGA	AAA	TAC	GGT	CTC	528
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	

165	170	175	
ACC GTA GAT AAT ACC ATC GAT GCA AGA ATG GTC GAC GTT AAT			570
Thr Val Asp Asn Thr Ile Asp Ala Arg Met Val Asp Val Asn			
180	185	190	
GGTATAATTG ATATCTCTAT TTTATATACT AATTAAATTT TATAGTGTGG ATCGGATAGT			630
GATTTTGGTC CATCAATTAA AAACCTGGTG AACATAAAAT TAACCAAGCA ATCAATTTAG			690
ACAAGCAACA TAATCATATA TATTTTTCTT ACATTTGTAT GTACCTGAAT ATTTATATTT			750
ATGTTTATAT GTTCTCACTA TATTTTCACT TTTGTATTTG AAAATTTTTA GGA AAA			806
		Gly Lys	
ATT TTG GAT AGA AAA TTG ATG GGA GAA GAT CTC TAC TGG GCA ATA AAC			854
Ile Leu Asp Arg Lys Leu Met Gly Glu Asp Leu Tyr Trp Ala Ile Asn			
195	200	205	
GGA GGA GGA GGA GGG AGC TAC GGC GTC GTA TTG GCC TAC AAA ATA AAC			902
Gly Gly Gly Gly Gly Ser Tyr Gly Val Val Leu Ala Tyr Lys Ile Asn			
210	215	220	
CTT GTT GAA GTC CCA GAA AAC GTC ACC GTT TTC AGA ATC TCC CGG ACG			950
Leu Val Glu Val Pro Glu Asn Val Thr Val Phe Arg Ile Ser Arg Thr			
225	230	235	240
TTA GAA CAA AAT GCG ACG GAT ATC ATT CAC CGG TGG CAA CAA GTT GCA			998
Leu Glu Gln Asn Ala Thr Asp Ile Ile His Arg Trp Gln Gln Val Ala			
245	250	255	
CCG AAG CTT CCC GAC GAG CTT TTC ATA AGA ACA GTC ATT GAC GTA GTA			1046
Pro Lys Leu Pro Asp Glu Leu Phe Ile Arg Thr Val Ile Asp Val Val			
260	265	270	
AAC GGC ACT GTT TCA TCT CAA AAG ACC GTC AGG ACA ACA TTC ATA GCA			1094
Asn Gly Thr Val Ser Ser Gln Lys Thr Val Arg Thr Thr Phe Ile Ala			
275	280	285	
ATG TTT CTA GGA GAC ACG ACA ACT CTA CTG TCG ATA TTA AAC CGG AGA			1142
Met Phe Leu Gly Asp Thr Thr Thr Leu Leu Ser Ile Leu Asn Arg Arg			
290	295	300	
TTC CCA GAA TTG GGT TTG GTC CGG TCT GAC TGT ACC GAA ACA AGC TGG			1190
Phe Pro Glu Leu Gly Leu Val Arg Ser Asp Cys Thr Glu Thr Ser Trp			
305	310	315	320
ATC CAA TCT GTG CTA TTC TGG ACA AAT ATC CAA GTT GGT TCG TCG GAG			1238
Ile Gln Ser Val Leu Phe Trp Thr Asn Ile Gln Val Gly Ser Ser Glu			
325	330	335	
ACA CTT CTA CTC CAA AGG AAT CAA CCC GTG AAC TAC CTC AAG AGG AAA			1286
Thr Leu Leu Leu Gln Arg Asn Gln Pro Val Asn Tyr Leu Lys Arg Lys			
340	345	350	

TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1334
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
		355					360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1382
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
		370				375					380					
TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TTA	CGG	GTG	ACT	CCG	TTC	CCA	1430
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Leu	Arg	Val	Thr	Pro	Phe	Pro	
		385				390				395					400	
TAC	AGA	GCC	GGT	AAT	CTC	TGG	AAG	ATT	CAG	TAC	GGT	GCG	AAT	TGG	AGA	1478
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg	
				405					410					415		
GAT	GAG	ACT	TTA	ACC	GAC	CGG	TAC	ATG	GAA	TTG	ACG	AGG	AAG	TTG	TAC	1526
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr	
			420					425					430			
CAA	TTC	ATG	ACA	CCA	TTT	GTT	TCC	AAG	AAT	CCG	AGA	CAA	TCG	TTT	TTC	1574
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe	
		435					440					445				
AAT	AAC	CGT	GAT	GTT	GAT	TTG	GGT	ATT	AAT	TCT	CAT	AAT	GGT	AAA	ATC	1622
Asn	Asn	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile	
		450				455					460					
AGT	AGT	TAT	GTG	GAA	GGT	AAA	CGT	TAC	GGG	AAG	AAG	TAT	TTC	GCA	GGT	1670
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly	
		465				470				475					480	
AAT	TTC	GAG	AGA	TTG	GTG	AAG	ATT	AAG	ACG	AGA	GTT	GAT	AGT	GGT	AAT	1718
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn	
				485				490						495		
TTC	TTT	AGG	AAC	GAA	CAC	AGT	ATT	CCT	GTG	TTA	CCA	TAA				1757
Phe	Phe	Arg	Asn	Glu	His	Ser	Ile	Pro	Val	Leu	Pro					
			500					505								

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn
1				5					10					15	

Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn		
			20						25					30			
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe		
		35					40					45					
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His		
	50					55					60						
Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu		
65					70					75					80		
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr		
				85					90					95			
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu		
			100					105					110				
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr		
		115					120					125					
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys		
	130					135					140						
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly		
145					150				155						160		
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu		
			165					170						175			
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys		
		180						185					190				
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn		
	195						200					205					
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn		
	210					215					220						
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr		
225					230					235				240			
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala		
			245					250						255			
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val		
		260						265					270				
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala		
	275					280					285						
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg		
	290					295				300							

Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp
305					310					315					320
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu
				325					330					335	
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys
			340					345					350		
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile
		355					360					365			
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro
	370					375					380				
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Leu	Arg	Val	Thr	Pro	Phe	Pro
385					390					395					400
Tyr	Arg	Ala	Gly	Asn	Leu	Trp	Lys	Ile	Gln	Tyr	Gly	Ala	Asn	Trp	Arg
			405						410					415	
Asp	Glu	Thr	Leu	Thr	Asp	Arg	Tyr	Met	Glu	Leu	Thr	Arg	Lys	Leu	Tyr
			420					425					430		
Gln	Phe	Met	Thr	Pro	Phe	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ser	Phe	Phe
		435						440				445			
Asn	Asn	Arg	Asp	Val	Asp	Leu	Gly	Ile	Asn	Ser	His	Asn	Gly	Lys	Ile
		450				455					460				
Ser	Ser	Tyr	Val	Glu	Gly	Lys	Arg	Tyr	Gly	Lys	Lys	Tyr	Phe	Ala	Gly
465					470					475					480
Asn	Phe	Glu	Arg	Leu	Val	Lys	Ile	Lys	Thr	Arg	Val	Asp	Ser	Gly	Asn
				485					490					495	
Phe	Phe	Arg	Asn	Glu	His	Ser	Ile	Pro	Val	Leu	Pro				
			500					505							

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(B) STRAIN: Colombia

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACT TCC CGT AGA AAC TCG GAG ACT TTC ACA CAA TGC CTA ACC TCA AAC	48
Thr Ser Arg Arg Asn Ser Glu Thr Phe Thr Gln Cys Leu Thr Ser Asn	
1 5 10 15	
TCC GAC CCC AAA CAT CCC ATC TCC CCC GCT ATC TTC TTC TCC GGA AAT	96
Ser Asp Pro Lys His Pro Ile Ser Pro Ala Ile Phe Phe Ser Gly Asn	
20 25 30	
GGC TCC TAC TCC TCC GTA TTA CAA GCC AAC ATC CGT AAC CTC CGC TTC	144
Gly Ser Tyr Ser Ser Val Leu Gln Ala Asn Ile Arg Asn Leu Arg Phe	
35 40 45	
AAC ACC ACC TCA ACT CCG AAA CCC TTC CTC ATA ATC GCC GCA ACA CAT	192
Asn Thr Thr Ser Thr Pro Lys Pro Phe Leu Ile Ile Ala Ala Thr His	
50 55 60	
GAA TCC CAT GTG CAA GCC GCG ATT ACT TGC GGG AAA CGC CAC AAC CTT	240
Glu Ser His Val Gln Ala Ala Ile Thr Cys Gly Lys Arg His Asn Leu	
65 70 75 80	
CAG ATG AAA ATC AGA AGT GGA GGC CAC GAC TAC GAT GGC TTG TCA TAC	288
Gln Met Lys Ile Arg Ser Gly Gly His Asp Tyr Asp Gly Leu Ser Tyr	
85 90 95	
GTT ACA TAC TCT GGC AAA CCG TTC TTC GTC CTC GAC ATG TTT AAC CTC	336
Val Thr Tyr Ser Gly Lys Pro Phe Phe Val Leu Asp Met Phe Asn Leu	
100 105 110	
CGT TCG GTG GAT GTC GAC GTG GCA AGT AAG ACC GCG TGG GTC CAA ACC	384
Arg Ser Val Asp Val Asp Val Ala Ser Lys Thr Ala Trp Val Gln Thr	
115 120 125	
GGT GCC ATA CTC GGA GAA GTT TAT TAC TAT ATA TGG GAG AAG AGC AAA	432
Gly Ala Ile Leu Gly Glu Val Tyr Tyr Tyr Ile Trp Glu Lys Ser Lys	
130 135 140	
ACC CTA GCT TAT CCC GCC GGA ATT TGT CCC ACG GTT GGT GTC GGT GGC	480
Thr Leu Ala Tyr Pro Ala Gly Ile Cys Pro Thr Val Gly Val Gly Gly	
145 150 155 160	
CAT ATC AGT GGT GGA GGT TAC GGT AAC ATG ATG AGA AAA TAC GGT CTC	528
His Ile Ser Gly Gly Gly Tyr Gly Asn Met Met Arg Lys Tyr Gly Leu	
165 170 175	

ACC	GTA	GAT	AAT	ACC	ATC	GAT	GCA	AGA	ATG	GTC	GAC	GTA	AAT	GGA	AAA	576
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	
			180					185					190			
ATT	TTG	GAT	AGA	AAA	TTG	ATG	GGA	GAA	GAT	CTC	TAC	TGG	GCA	ATA	AAC	624
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	
		195					200					205				
GGA	GGA	GGA	GGA	GGG	AGC	TAC	GGC	GTC	GTA	TTG	GCC	TAC	AAA	ATA	AAC	672
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	
	210					215					220					
CTT	GTT	GAA	GTC	CCA	GAA	AAC	GTC	ACC	GTT	TTC	AGA	ATC	TCC	CGG	ACG	720
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	
225					230					235					240	
TTA	GAA	CAA	AAT	GCG	ACG	GAT	ATC	ATT	CAC	CGG	TGG	CAA	CAA	GTT	GCA	768
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	
			245					250						255		
CCG	AAG	CTT	CCC	GAC	GAG	CTT	TTC	ATA	AGA	ACA	GTC	ATT	GAC	GTA	GTA	816
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	
		260						265					270			
AAC	GGC	ACT	GTT	TCA	TCT	CAA	AAG	ACC	GTC	AGG	ACA	ACA	TTC	ATA	GCA	864
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	
	275						280					285				
ATG	TTT	CTA	GGA	GAC	ACG	ACA	ACT	CTA	CTG	TCG	ATA	TTA	AAC	CGG	AGA	912
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	
	290					295					300					
TTC	CCA	GAA	TTG	GGT	TTG	GTC	CGG	TCT	GAC	TGT	ACC	GAA	ACA	AGC	TGG	960
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	
305				310						315					320	
ATC	CAA	TCT	GTG	CTA	TTC	TGG	ACA	AAT	ATC	CAA	GTT	GGT	TCG	TCG	GAG	1008
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	
			325					330						335		
ACA	CTT	CTA	CTC	CAA	AGG	AAT	CAA	CCC	GTG	AAC	TAC	CTC	AAG	AGG	AAA	1056
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	
		340					345						350			
TCA	GAT	TAC	GTA	CGT	GAA	CCG	ATT	TCA	AGA	ACC	GGT	TTA	GAG	TCA	ATT	1104
Ser	Asp	Tyr	Val	Arg	Glu	Pro	Ile	Ser	Arg	Thr	Gly	Leu	Glu	Ser	Ile	
	355						360					365				
TGG	AAG	AAA	ATG	ATC	GAG	CTT	GAA	ATT	CCG	ACA	ATG	GCT	TTC	AAT	CCA	1152
Trp	Lys	Lys	Met	Ile	Glu	Leu	Glu	Ile	Pro	Thr	Met	Ala	Phe	Asn	Pro	
	370					375					380					
TAC	GGT	GGT	GAG	ATG	GGG	AGG	ATA	TCA	TCT	ACG	GTG	ACT	CCG	TTC	CCA	1200
Tyr	Gly	Gly	Glu	Met	Gly	Arg	Ile	Ser	Ser	Thr	Val	Thr	Pro	Phe	Pro	

385	390	395	400	
TAC AGA GCC GGT AAT CTC TGG AAG ATT CAG TAC GGT GCG AAT TGG AGA	1248			
Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg				
405	410	415		
GAT GAG ACT TTA ACC GAC CGG TAC ATG GAA TTG ACG AGG AAG TTG TAC	1296			
Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr				
420	425	430		
CAA TTC ATG ACA CCA TTT GTT TCC AAG AAT CCG AGA CAA TCG TTT TTC	1344			
Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe				
435	440	445		
AAT TAC CGT GAT GTT GAT TTG GGT ATT AAT TCT CAT AAT GGT AAA ATC	1392			
Asn Tyr Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile				
450	455	460		
AGT AGT TAT GTG GAA GGT AAA CGT TAC GGG AAG AAG TAT TTC GCA GGT	1440			
Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly				
465	470	475	480	
AAT TTC GAG AGA TTG GTG AAG ATT AAG ACG AGA GTT GAT AGT GGT AAT	1488			
Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn				
485	490	495		
TTC TTT AGG AAC GAA CAG AGT ATT CCT GTG TTA CCA TAA	1527			
Phe Phe Arg Asn Glu Gln Ser Ile Pro Val Leu Pro				
500	505			

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Thr	Ser	Arg	Arg	Asn	Ser	Glu	Thr	Phe	Thr	Gln	Cys	Leu	Thr	Ser	Asn
1				5					10					15	
Ser	Asp	Pro	Lys	His	Pro	Ile	Ser	Pro	Ala	Ile	Phe	Phe	Ser	Gly	Asn
			20					25					30		
Gly	Ser	Tyr	Ser	Ser	Val	Leu	Gln	Ala	Asn	Ile	Arg	Asn	Leu	Arg	Phe
		35					40					45			
Asn	Thr	Thr	Ser	Thr	Pro	Lys	Pro	Phe	Leu	Ile	Ile	Ala	Ala	Thr	His
	50					55					60				

Glu	Ser	His	Val	Gln	Ala	Ala	Ile	Thr	Cys	Gly	Lys	Arg	His	Asn	Leu	
65					70					75					80	
Gln	Met	Lys	Ile	Arg	Ser	Gly	Gly	His	Asp	Tyr	Asp	Gly	Leu	Ser	Tyr	
				85					90					95		
Val	Thr	Tyr	Ser	Gly	Lys	Pro	Phe	Phe	Val	Leu	Asp	Met	Phe	Asn	Leu	
			100					105					110			
Arg	Ser	Val	Asp	Val	Asp	Val	Ala	Ser	Lys	Thr	Ala	Trp	Val	Gln	Thr	
		115					120					125				
Gly	Ala	Ile	Leu	Gly	Glu	Val	Tyr	Tyr	Tyr	Ile	Trp	Glu	Lys	Ser	Lys	
	130					135					140					
Thr	Leu	Ala	Tyr	Pro	Ala	Gly	Ile	Cys	Pro	Thr	Val	Gly	Val	Gly	Gly	
145					150					155					160	
His	Ile	Ser	Gly	Gly	Gly	Tyr	Gly	Asn	Met	Met	Arg	Lys	Tyr	Gly	Leu	
			165					170						175		
Thr	Val	Asp	Asn	Thr	Ile	Asp	Ala	Arg	Met	Val	Asp	Val	Asn	Gly	Lys	
		180						185					190			
Ile	Leu	Asp	Arg	Lys	Leu	Met	Gly	Glu	Asp	Leu	Tyr	Trp	Ala	Ile	Asn	
		195					200					205				
Gly	Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Val	Val	Leu	Ala	Tyr	Lys	Ile	Asn	
	210					215					220					
Leu	Val	Glu	Val	Pro	Glu	Asn	Val	Thr	Val	Phe	Arg	Ile	Ser	Arg	Thr	
225					230					235					240	
Leu	Glu	Gln	Asn	Ala	Thr	Asp	Ile	Ile	His	Arg	Trp	Gln	Gln	Val	Ala	
				245					250					255		
Pro	Lys	Leu	Pro	Asp	Glu	Leu	Phe	Ile	Arg	Thr	Val	Ile	Asp	Val	Val	
			260					265					270			
Asn	Gly	Thr	Val	Ser	Ser	Gln	Lys	Thr	Val	Arg	Thr	Thr	Phe	Ile	Ala	
		275					280					285				
Met	Phe	Leu	Gly	Asp	Thr	Thr	Thr	Leu	Leu	Ser	Ile	Leu	Asn	Arg	Arg	
	290					295					300					
Phe	Pro	Glu	Leu	Gly	Leu	Val	Arg	Ser	Asp	Cys	Thr	Glu	Thr	Ser	Trp	
305					310					315					320	
Ile	Gln	Ser	Val	Leu	Phe	Trp	Thr	Asn	Ile	Gln	Val	Gly	Ser	Ser	Glu	
				325					330					335		
Thr	Leu	Leu	Leu	Gln	Arg	Asn	Gln	Pro	Val	Asn	Tyr	Leu	Lys	Arg	Lys	
			340				345						350			

Ser Asp Tyr Val Arg Glu Pro Ile Ser Arg Thr Gly Leu Glu Ser Ile
 355 360 365
 Trp Lys Lys Met Ile Glu Leu Glu Ile Pro Thr Met Ala Phe Asn Pro
 370 375 380
 Tyr Gly Gly Glu Met Gly Arg Ile Ser Ser Thr Val Thr Pro Phe Pro
 385 390 395 400
 Tyr Arg Ala Gly Asn Leu Trp Lys Ile Gln Tyr Gly Ala Asn Trp Arg
 405 410 415
 Asp Glu Thr Leu Thr Asp Arg Tyr Met Glu Leu Thr Arg Lys Leu Tyr
 420 425 430
 Gln Phe Met Thr Pro Phe Val Ser Lys Asn Pro Arg Gln Ser Phe Phe
 435 440 445
 Asn Tyr Arg Asp Val Asp Leu Gly Ile Asn Ser His Asn Gly Lys Ile
 450 455 460
 Ser Ser Tyr Val Glu Gly Lys Arg Tyr Gly Lys Lys Tyr Phe Ala Gly
 465 470 475 480
 Asn Phe Glu Arg Leu Val Lys Ile Lys Thr Arg Val Asp Ser Gly Asn
 485 490 495
 Phe Phe Arg Asn Glu Gln Ser Ile Pro Val Leu Pro
 500 505

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (B) STRAIN: Colombia
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCC	ATC	CAA	GAT	CAA	TTC	ATA	AAC	TGT	GTC	AAA	AGA	AAC	ACA	CAT	GTT	48
Ser	Ile	Gln	Asp	Gln	Phe	Ile	Asn	Cys	Val	Lys	Arg	Asn	Thr	His	Val	
1				5					10					15		
TCT	TTT	CCA	CTC	GAG	AAA	ACG	TTA	TTC	ACC	CCT	GCG	AAA	AAC	GTC	TCT	96
Ser	Phe	Pro	Leu	Glu	Lys	Thr	Leu	Phe	Thr	Pro	Ala	Lys	Asn	Val	Ser	
			20					25					30			
TTG	TTC	AAC	CAA	GTC	CTT	GAA	TCG	ACG	GCT	CAA	AAT	CTC	CAG	TTC	TTG	144
Leu	Phe	Asn	Gln	Val	Leu	Glu	Ser	Thr	Ala	Gln	Asn	Leu	Gln	Phe	Leu	
		35					40					45				
GCA	AAA	TCC	ATG	CCT	AAA	CCG	GGA	TTC	ATA	TTC	AGA	CCG	ATT	CAC	CAG	192
Ala	Lys	Ser	Met	Pro	Lys	Pro	Gly	Phe	Ile	Phe	Arg	Pro	Ile	His	Gln	
	50					55					60					
TCT	CAA	GTC	CAA	GCT	TCC	ATC	ATT	TGT	TCA	AAG	AAA	CTC	GGA	ATT	CAT	240
Ser	Gln	Val	Gln	Ala	Ser	Ile	Ile	Cys	Ser	Lys	Lys	Leu	Gly	Ile	His	
65					70				75					80		
TTT	CGT	GTT	AGA	AGT	GGC	GGT	CAC	GAT	TTC	GAG	GCC	TTG	TCT	TAT	GTT	288
Phe	Arg	Val	Arg	Ser	Gly	Gly	His	Asp	Phe	Glu	Ala	Leu	Ser	Tyr	Val	
				85					90					95		
TCA	CGG	ATT	GAA	AAA	CCG	TTT	ATA	TTA	CTC	GAC	CTG	TCA	AAA	TTG	AAA	336
Ser	Arg	Ile	Glu	Lys	Pro	Phe	Ile	Leu	Leu	Asp	Leu	Ser	Lys	Leu	Lys	
			100					105					110			
CAA	ATC	AAT	GTT	GAT	ATT	GAA	TCC	AAT	AGT	GCT	TGG	GTT	CAA	CCT	GGT	384
Gln	Ile	Asn	Val	Asp	Ile	Glu	Ser	Asn	Ser	Ala	Trp	Val	Gln	Pro	Gly	
		115					120					125				
GCT	ACG	CTT	GGT	GAG	CTT	TAC	TAC	AGA	ATT	GCA	GAG	AAG	AGC	AAG	ATC	432
Ala	Thr	Leu	Gly	Glu	Leu	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Lys	Ile	
	130					135					140					
CAT	GGA	TTT	CCC	GCG	GGT	TTG	TGC	ACA	AGT	GTA	GGC	ATA	GGT	GGG	TAT	480
His	Gly	Phe	Pro	Ala	Gly	Leu	Cys	Thr	Ser	Val	Gly	Ile	Gly	Gly	Tyr	
145					150					155				160		
ATG	ACA	GGC	GGT	GGA	TAC	GGT	ACC	TTG	ATG	AGG	AAG	TAT	GGT	CTT	GCG	528
Met	Thr	Gly	Gly	Gly	Tyr	Gly	Thr	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ala	
				165				170						175		
GGA	GAT	AAT	GTT	CTA	GAC	GTA	AAG	ATG	GTT	GAT	GCA	AAT	GGT	AAA	TTA	576
Gly	Asp	Asn	Val	Leu	Asp	Val	Lys	Met	Val	Asp	Ala	Asn	Gly	Lys	Leu	
			180					185					190			
CTC	GAC	AGA	GCC	GCG	ATG	GGT	GAG	GAC	CTA	TTT	TGG	GCG	ATT	AGA	GGA	624
Leu	Asp	Arg	Ala	Ala	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Arg	Gly	
		195					200					205				

GGC	GGT	GGA	GCG	AGT	TTC	GGG	ATA	GTT	CTA	GCA	TGG	AAG	ATC	AAG	CTT	672
Gly	Gly	Gly	Ala	Ser	Phe	Gly	Ile	Val	Leu	Ala	Trp	Lys	Ile	Lys	Leu	
	210						215				220					
GTT	CCT	GTT	CCT	AAG	ACT	GTT	ACC	GTC	TTC	ACT	GTC	ACC	AAA	ACG	TTA	720
Val	Pro	Val	Pro	Lys	Thr	Val	Thr	Val	Phe	Thr	Val	Thr	Lys	Thr	Leu	
	225						230				235				240	
GAA	CAA	GAC	GCA	AGA	TTG	AAG	ACT	ATT	TCT	AAG	TGG	CAA	CAA	ATT	TCA	768
Glu	Gln	Asp	Ala	Arg	Leu	Lys	Thr	Ile	Ser	Lys	Trp	Gln	Gln	Ile	Ser	
				245						250					255	
TCC	AAG	ATT	ATT	GAA	GAG	ATA	CAC	ATC	CGA	GTG	GTA	CTC	AGA	GCA	GCT	816
Ser	Lys	Ile	Ile	Glu	Glu	Ile	His	Ile	Arg	Val	Val	Leu	Arg	Ala	Ala	
			260						265					270		
GGA	AAT	GAT	GGA	AAC	AAG	ACT	GTG	ACA	ATG	ACC	TAC	CTA	GGT	CAG	TTT	864
Gly	Asn	Asp	Gly	Asn	Lys	Thr	Val	Thr	Met	Thr	Tyr	Leu	Gly	Gln	Phe	
		275						280					285			
CTT	GGC	GAG	AAA	GGC	ACC	TTG	CTG	AAG	GTT	ATG	GAG	AAG	GCT	TTT	CCA	912
Leu	Gly	Glu	Lys	Gly	Thr	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Phe	Pro	
	290						295					300				
GAA	CTA	GGG	TTA	ACT	CAA	AAG	GAT	TGT	ACT	GAA	ATG	AGC	TGG	ATT	GAA	960
Glu	Leu	Gly	Leu	Thr	Gln	Lys	Asp	Cys	Thr	Glu	Met	Ser	Trp	Ile	Glu	
	305					310					315				320	
GCC	GCC	CTT	TTC	CAT	GGT	GGA	TTT	CCA	ACA	GGT	TCT	CCT	ATT	GAA	ATT	1008
Ala	Ala	Leu	Phe	His	Gly	Gly	Phe	Pro	Thr	Gly	Ser	Pro	Ile	Glu	Ile	
				325					330					335		
TTG	CTT	CAG	CTC	AAG	TCG	CCT	CTA	GGA	AAA	GAT	TAC	TTC	AAA	GCA	ACG	1056
Leu	Leu	Gln	Leu	Lys	Ser	Pro	Leu	Gly	Lys	Asp	Tyr	Phe	Lys	Ala	Thr	
			340						345					350		
TCG	GAT	TTC	GTT	AAA	GAA	CCT	ATT	CCT	GTG	ATA	GGC	TTC	AAA	GGA	ATA	1104
Ser	Asp	Phe	Val	Lys	Glu	Pro	Ile	Pro	Val	Ile	Gly	Phe	Lys	Gly	Ile	
		355						360					365			
TTC	AAA	AGA	TTG	ATT	GAA	GGA	AAC	ACA	ACA	TTT	CTG	AAC	TGG	ACT	CCT	1152
Phe	Lys	Arg	Leu	Ile	Glu	Gly	Asn	Thr	Thr	Phe	Leu	Asn	Trp	Thr	Pro	
	370						375					380				
TAC	GGT	GGT	ATG	ATG	TCG	AAA	ATC	CCT	GAA	TCT	GCG	ATC	CCA	TTT	CCG	1200
Tyr	Gly	Gly	Met	Met	Ser	Lys	Ile	Pro	Glu	Ser	Ala	Ile	Pro	Phe	Pro	
	385					390					395				400	
CAT	AGA	AAC	GGA	ACC	CTC	TTC	AAG	ATT	CTC	TAT	TAC	GCG	AAC	TGG	CTA	1248
His	Arg	Asn	Gly	Thr	Leu	Phe	Lys	Ile	Leu	Tyr	Tyr	Ala	Asn	Trp	Leu	
				405						410					415	

GAG AAT GAC AAG ACA TCG AGT AGA AAA ATC AAC TGG ATC AAA GAG ATA 1296
 Glu Asn Asp Lys Thr Ser Ser Arg Lys Ile Asn Trp Ile Lys Glu Ile
 420 425 430

TAC AAT TAC ATG GCG CCT TAT GTC TCA AGC AAT CCA AGA CAA GCA TAT 1344
 Tyr Asn Tyr Met Ala Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr
 435 440 445

GTG AAC TAC AGA GAT CTA GAC TTC GGA CAG AAC AAG AAC AAC GCA AAG 1392
 Val Asn Tyr Arg Asp Leu Asp Phe Gly Gln Asn Lys Asn Asn Ala Lys
 450 455 460

GTT AAC TTC ATT GAA GCT AAA ATC TGG GGA CCT AAG TAC TTC AAA GGC 1440
 Val Asn Phe Ile Glu Ala Lys Ile Trp Gly Pro Lys Tyr Phe Lys Gly
 465 470 475 480

AAT TTT GAC AGA TTG GTG AAG ATT AAA ACC AAG GTT GAT CCA GAG AAC 1488
 Asn Phe Asp Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn
 485 490 495

TTC TTC AGG CAC GAG CAG AGT ATC CCA CCT ATG CCC TAC TAG 1530
 Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ser Ile Gln Asp Gln Phe Ile Asn Cys Val Lys Arg Asn Thr His Val
 1 5 10 15

Ser Phe Pro Leu Glu Lys Thr Leu Phe Thr Pro Ala Lys Asn Val Ser
 20 25 30

Leu Phe Asn Gln Val Leu Glu Ser Thr Ala Gln Asn Leu Gln Phe Leu
 35 40 45

Ala Lys Ser Met Pro Lys Pro Gly Phe Ile Phe Arg Pro Ile His Gln
 50 55 60

Ser Gln Val Gln Ala Ser Ile Ile Cys Ser Lys Lys Leu Gly Ile His
 65 70 75 80

Phe Arg Val Arg Ser Gly Gly His Asp Phe Glu Ala Leu Ser Tyr Val
 85 90 95

Ser Arg Ile Glu Lys Pro Phe Ile Leu Leu Asp Leu Ser Lys Leu Lys

100					105					110					
Gln	Ile	Asn	Val	Asp	Ile	Glu	Ser	Asn	Ser	Ala	Trp	Val	Gln	Pro	Gly
		115					120					125			
Ala	Thr	Leu	Gly	Glu	Leu	Tyr	Tyr	Arg	Ile	Ala	Glu	Lys	Ser	Lys	Ile
	130					135					140				
His	Gly	Phe	Pro	Ala	Gly	Leu	Cys	Thr	Ser	Val	Gly	Ile	Gly	Gly	Tyr
145					150					155					160
Met	Thr	Gly	Gly	Gly	Tyr	Gly	Thr	Leu	Met	Arg	Lys	Tyr	Gly	Leu	Ala
				165					170					175	
Gly	Asp	Asn	Val	Leu	Asp	Val	Lys	Met	Val	Asp	Ala	Asn	Gly	Lys	Leu
			180					185					190		
Leu	Asp	Arg	Ala	Ala	Met	Gly	Glu	Asp	Leu	Phe	Trp	Ala	Ile	Arg	Gly
		195					200					205			
Gly	Gly	Gly	Ala	Ser	Phe	Gly	Ile	Val	Leu	Ala	Trp	Lys	Ile	Lys	Leu
	210					215					220				
Val	Pro	Val	Pro	Lys	Thr	Val	Thr	Val	Phe	Thr	Val	Thr	Lys	Thr	Leu
225					230					235					240
Glu	Gln	Asp	Ala	Arg	Leu	Lys	Thr	Ile	Ser	Lys	Trp	Gln	Gln	Ile	Ser
			245						250					255	
Ser	Lys	Ile	Ile	Glu	Glu	Ile	His	Ile	Arg	Val	Val	Leu	Arg	Ala	Ala
			260					265					270		
Gly	Asn	Asp	Gly	Asn	Lys	Thr	Val	Thr	Met	Thr	Tyr	Leu	Gly	Gln	Phe
		275					280					285			
Leu	Gly	Glu	Lys	Gly	Thr	Leu	Leu	Lys	Val	Met	Glu	Lys	Ala	Phe	Pro
	290					295					300				
Glu	Leu	Gly	Leu	Thr	Gln	Lys	Asp	Cys	Thr	Glu	Met	Ser	Trp	Ile	Glu
305					310					315					320
Ala	Ala	Leu	Phe	His	Gly	Gly	Phe	Pro	Thr	Gly	Ser	Pro	Ile	Glu	Ile
				325					330					335	
Leu	Leu	Gln	Leu	Lys	Ser	Pro	Leu	Gly	Lys	Asp	Tyr	Phe	Lys	Ala	Thr
			340					345					350		
Ser	Asp	Phe	Val	Lys	Glu	Pro	Ile	Pro	Val	Ile	Gly	Phe	Lys	Gly	Ile
		355					360					365			
Phe	Lys	Arg	Leu	Ile	Glu	Gly	Asn	Thr	Thr	Phe	Leu	Asn	Trp	Thr	Pro
	370					375					380				
Tyr	Gly	Gly	Met	Met	Ser	Lys	Ile	Pro	Glu	Ser	Ala	Ile	Pro	Phe	Pro

385 390 395 400
 His Arg Asn Gly Thr Leu Phe Lys Ile Leu Tyr Tyr Ala Asn Trp Leu
 405 410 415
 Glu Asn Asp Lys Thr Ser Ser Arg Lys Ile Asn Trp Ile Lys Glu Ile
 420 425 430
 Tyr Asn Tyr Met Ala Pro Tyr Val Ser Ser Asn Pro Arg Gln Ala Tyr
 435 440 445
 Val Asn Tyr Arg Asp Leu Asp Phe Gly Gln Asn Lys Asn Asn Ala Lys
 450 455 460
 Val Asn Phe Ile Glu Ala Lys Ile Trp Gly Pro Lys Tyr Phe Lys Gly
 465 470 475 480
 Asn Phe Asp Arg Leu Val Lys Ile Lys Thr Lys Val Asp Pro Glu Asn
 485 490 495
 Phe Phe Arg His Glu Gln Ser Ile Pro Pro Met Pro Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met Glu Asn Lys Thr Pro Ile Phe Phe Ser Leu Ser Ile Phe Leu Ser
 1 5 10 15
 Leu Leu Asn Cys Ala Leu Gly Gly Asn Asp Leu Leu Ser Cys Leu Thr
 20 25 30
 Phe Asn Gly Val Arg Asn His Thr Val Phe Ser Ala Asp Ser Asp Ser
 35 40 45
 Asp Phe Asn Arg Phe Leu His Leu Ser Ile Gln Asn Pro Leu Phe Gln
 50 55 60
 Asn Ser Leu Ile Ser Lys Pro Ser Ala Ile Ile Leu Pro Gly Ser Lys
 65 70 75 80

Glu Glu Leu Ser Asn Thr Ile Arg Cys Ile Arg Lys Gly Ser Trp Thr
85 90 95

Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly Leu Ser Tyr Thr
100 105 110

Ser Asp Thr Pro Phe Ile Leu Ile Asp Leu Met Asn Leu Asn Arg Val
115 120 125

Ser Ile Asp Leu Glu Ser Glu Thr Ala Trp Val Glu Ser Gly Ser Thr
130 135 140

Leu Gly Glu Leu Tyr Tyr Ala Ile Thr Glu Ser Ser Ser Lys Leu Gly
145 150 155 160

Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Thr Gly Gly His Ile Ser
165 170 175

Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly Leu Ala Ala Asp
180 185 190

Asn Val Val Asp Ala Ile Leu Ile Asp Ala Asn Gly Ala Ile Leu Asp
195 200 205

Arg Gln Ala Met Gly Glu Asp Val Phe Trp Ala Ile Arg Gly Gly Gly
210 215 220

Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile Lys Leu Leu Pro
225 230 235 240

Val Pro Glu Lys Val Thr Val Phe Arg Val Thr Lys Asn Val Ala Ile
245 250 255

Asp Glu Ala Thr Ser Leu Leu His Lys Trp Gln Phe Val Ala Glu Glu
260 265 270

Leu Glu Glu Asp Phe Thr Leu Ser Val Leu Gly Gly Ala Asp Glu Lys
275 280 285

Gln Val Trp Leu Thr Met Leu Gly Phe His Phe Gly Leu Lys Thr Val
290 295 300

Ala Lys Ser Thr Phe Asp Leu Leu Phe Pro Glu Leu Gly Leu Val Glu
305 310 315 320

Glu Asp Tyr Leu Glu Met Ser Trp Gly Glu Ser Phe Ala Tyr Leu Ala
325 330 335

Gly Leu Glu Thr Val Ser Gln Leu Asn Asn Arg Phe Leu Lys Phe Asp
340 345 350

Glu Arg Ala Phe Lys Thr Lys Val Asp Leu Thr Lys Glu Pro Leu Pro
355 360 365

Ser Lys Ala Phe Tyr Gly Gly Leu Leu Glu Arg Leu Ser Lys Glu Pro
370 375 380

Asn Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Gln Met Ser Lys Ile
385 390 395 400

Ser Ser Asp Phe Thr Pro Phe Pro His Arg Ser Gly Thr Arg Leu Met
405 410 415

Val Glu Tyr Ile Val Ala Trp Asn Gln Ser Glu Gln Lys Lys Lys Thr
420 425 430

Glu Phe Leu Asp Trp Leu Glu Lys Val Tyr Glu Phe Met Lys Pro Phe
435 440 445

Val Ser Lys Asn Pro Arg Leu Gly Tyr Val Asn His Ile Asp Leu Asp
450 455 460

Leu Gly Gly Ile Asp Trp Gly Asn Lys Thr Val Val Asn Asn Ala Ile
465 470 475 480

Glu Ile Ser Arg Ser Trp Gly Glu Ser Tyr Phe Leu Ser Asn Tyr Glu
485 490 495

Arg Leu Ile Arg Ala Lys Thr Leu Ile Asp Pro Asn Asn Val Phe Asn
500 505 510

His Pro Gln Ser Ile Pro Pro Met Ala Asn Phe Asp Tyr Leu Glu Lys

515

520

525

Thr Leu Gly Ser Asp Gly Gly Glu Val Val Ile
 530 535

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 536 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met Met Cys Arg Ser Leu Thr Leu Arg Phe Phe Leu Phe Ile Val Leu
 1 5 10 15

Leu Gln Thr Cys Val Arg Gly Gly Asp Val Asn Asp Asn Leu Leu Ser
 20 25 30

Ser Cys Leu Asn Ser His Gly Val His Asn Phe Thr Thr Leu Ser Thr
 35 40 45

Asp Thr Asn Ser Asp Tyr Phe Lys Leu Leu His Ala Ser Met Gln Asn
 50 55 60

Pro Leu Phe Ala Lys Pro Thr Val Ser Lys Pro Ser Phe Ile Val Met
 65 70 75 80

Pro Gly Ser Lys Glu Glu Leu Ser Ser Thr Val His Cys Cys Thr Arg
 85 90 95

Glu Ser Trp Thr Ile Arg Leu Arg Ser Gly Gly His Ser Tyr Glu Gly
 100 105 110

Leu Ser Tyr Thr Ala Asp Thr Pro Phe Val Ile Val Asp Met Met Asn
 115 120 125

Leu Asn Arg Ile Ser Ile Asp Val Leu Ser Glu Thr Ala Trp Val Glu

130		135		140
Ser Gly Ala Thr Leu Gly Glu Leu Tyr Tyr Ala Ile Ala Gln Ser Thr				
145		150		155
				160
Asp Thr Leu Gly Phe Thr Ala Gly Trp Cys Pro Thr Val Gly Ser Gly				
	165		170	175
Gly His Ile Ser Gly Gly Gly Phe Gly Met Met Ser Arg Lys Tyr Gly				
	180		185	190
Leu Ala Ala Asp Asn Val Val Asp Ala Ile Leu Ile Asp Ser Asn Gly				
	195		200	205
Ala Ile Leu Asp Arg Glu Lys Met Gly Asp Asp Val Phe Trp Ala Ile				
	210		215	220
Arg Gly Gly Gly Gly Gly Val Trp Gly Ala Ile Tyr Ala Trp Lys Ile				
225		230		235
				240
Lys Leu Leu Pro Val Pro Glu Lys Leu Thr Val Phe Arg Val Thr Lys				
	245		250	255
Asn Val Gly Ile Glu Asp Ala Ser Ser Leu Leu His Lys Trp Gln Tyr				
	260		265	270
Val Ala Asp Glu Leu Asp Glu Asp Phe Thr Val Ser Val Leu Gly Gly				
	275		280	285
Val Asn Gly Asn Asp Ala Trp Leu Met Phe Leu Gly Leu His Leu Gly				
	290		295	300
Arg Lys Asp Ala Ala Lys Thr Ile Ile Asp Glu Lys Phe Pro Glu Leu				
305		310		315
				320
Gly Leu Val Asp Lys Glu Phe Gln Glu Met Ser Trp Gly Glu Ser Met				
	325		330	335
Ala Phe Leu Ser Gly Leu Asp Thr Ile Ser Glu Leu Asn Asn Arg Phe				
	340		345	350

Leu Lys Phe Asp Glu Arg Ala Phe Lys Thr Lys Val Asp Phe Thr Lys
355 360 365

Val Ser Val Pro Leu Asn Val Phe Arg His His Ala Leu Glu Met Leu
370 375 380

Ser Glu Gln Pro Gly Gly Phe Ile Ala Leu Asn Gly Phe Gly Gly Lys
385 390 395 400

Met Ser Glu Ile Ser Thr Asp Phe Thr Pro Phe Pro His Arg Lys Gly
405 410 415

Thr Lys Leu Met Phe Glu Tyr Ile Ile Ala Trp Asn Gln Asp Glu Glu
420 425 430

Ser Lys Ile Gly Glu Phe Ser Glu Trp Leu Ala Lys Phe Tyr Asp Tyr
435 440 445

Leu Glu Pro Phe Val Ser Lys Glu Pro Arg Val Gly Tyr Val Asn His
450 455 460

Ile Asp Leu Asp Ile Gly Gly Ile Asp Trp Arg Asn Lys Ser Ser Thr
465 470 475 480

Thr Asn Ala Val Glu Ile Ala Arg Asn Trp Gly Glu Arg Tyr Phe Ser
485 490 495

Ser Asn Tyr Glu Arg Leu Val Lys Ala Lys Thr Leu Ile Asp Pro Asn
500 505 510

Asn Val Phe Asn His Pro Gln Ser Ile Pro Pro Met Met Lys Phe Glu
515 520 525

Glu Ile Tyr Met Leu Lys Glu Leu
530 535